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# HUMAN xiap

SEQ ID NO:3	1	gaaaagggtggacaagtcctaatttcaagagaagatgacttttaacagttttgaaggatctt	60
SEQ ID NO:4 a		M T F N S F E G S	-
	61	aaaacttgtgtacctgcagacatcaataaggaagaattttagaagagtttaataaga	120
a		K T C V P A D I N K E E F V E E F N R	-
	121	ttaaaaaacttttgctaattttccaagtggtagtcctgtttcagcatcaacactggcacga	180
a		L K T F A N F P S G S P V S A S T L A R	-
	181	gcagggttcttatactggtgaaggagataccgtgcggtgctttagttgtcatgcagct	240
a		A G F L Y T G E G D T V R C F S C H A A	-
	241	gtagatagatggcaatatggagactcagcagttggaagacacaggaagatccccaaat	300
a		V D R W Q Y G D S A V G R H R K V S P N	-
	301	tgcagatttatcaacggcttttatcttgaaaaatagtgccacgcagtcctacaaattctggt	360
a		C R F I N G F Y L E N S A T Q S T N S G	-

Fig. 1 (page 1 of 7)

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# HUMAN xiap

```
361 atccagaatggtcagtacaaagttagaaactatctgggaagcagagatcattttgcctta 420
-----+-----+-----+
a I Q N G Q Y K V E N Y L G S R D H F A L -

421 gacaggccatctgagacacatgcagactatcttttgagaactgggcagggttagatatata 480
-----+-----+-----+
a D R P S E T H A D Y L L R T G Q V V D I -

481 tcagacacatataccggaggaaacctgccatgtattgtgaagaagctagattaaagtcc 540
-----+-----+-----+
a S D T I Y P R N P A M Y C E E A R L K S -

541 tttcagaactggccagactatgctcacctaaccccaagagagtagcaagtgtgactc 600
-----+-----+-----+
a F Q N W P D Y A H L T P R E L A S A G L -

601 tactacacagggtattggtgaccaagtgcagtgcttttgttgggtgaaaactgaaaaat 660
-----+-----+-----+
a Y Y T G I G D Q V Q C F C C G G K L K N -

661 tgggaaccttgtgatcgctgcctggtcagaacacacaggcgacactttcctaattgcttcttt 720
-----+-----+-----+
a W E P C D R A W S E H R R R H F P N C F F -
```

Fig. 1 (page 2 of 7)

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# HUMAN xiap

```

721      gtttggcggaatcttaataattcgaagtgaatctgatgctgtgagttctgataggaat 780
      -----+-----+-----+-----+-----+-----+-----+
a      V L G R N L N I R S E S D A V S S D R N -
      -----+-----+-----+-----+-----+-----+-----+
781      ttcccaaatccaacaatcttccaagaaatcccatcccatggcagattatgaagcacggatc 840
      -----+-----+-----+-----+-----+-----+-----+
a      F P N S T N L P R N P S M A D Y E A R I -
      -----+-----+-----+-----+-----+-----+-----+
841      ttacttttgggacatggatataactcagtttaacaaggagcagcttgcaagagctggattt 900
      -----+-----+-----+-----+-----+-----+-----+
a      F T F G T W I Y S V N K E Q L A R A G F -
      -----+-----+-----+-----+-----+-----+-----+
901      tatgcttttaggtgaagtgataaaagtaaagtcttctcactgtggaggaggctaaactgat 960
      -----+-----+-----+-----+-----+-----+-----+
a      Y A L G E G D K V K C F H C G G G L T D -
      -----+-----+-----+-----+-----+-----+-----+
961      tggaagcccagtgaagacccttggaacaacatgctaaatggtatccagggtgcaaatat 1020
      -----+-----+-----+-----+-----+-----+-----+
a      W K P S E D P W E Q H A K W Y P G C K Y -
      -----+-----+-----+-----+-----+-----+-----+
1021     ctgtagaacagaaggacagaataataaacaatatctcatttaactcattcacttgag 1080
      -----+-----+-----+-----+-----+-----+-----+
a      L L E Q K G Q E Y I N N I H L T H S L E -
      -----+-----+-----+-----+-----+-----+-----+

```

Fig. 1 (page 3 of 7)

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# HUMAN xiap

```
1081      gagtgtctggaactactgagaaacaccatcactaactagaagaattgatgatacc 1140
      -----+-----+-----+-----+-----+
a      E C L V R T T E K T P S L T R R I D D T -
      -----+-----+-----+-----+-----+
1141      atcttccaaaatcctatggtacaagaagctatacgaatggggttcagtttcaaggacatt 1200
      -----+-----+-----+-----+-----+
a      I F Q N P M V Q E A I R M G F S F K D I -
      -----+-----+-----+-----+-----+
1201      aagaaaaataatggaggaaaaaattcagatatctctgggagcaactataaaatcacttgaggtt 1260
      -----+-----+-----+-----+-----+
a      K K I M E E K I Q I S G S N Y K S L E V -
      -----+-----+-----+-----+-----+
1261      ctggttgcagatctagtgaatgctcagaaaagacagtatgcaagatgagtcagtcagact 1320
      -----+-----+-----+-----+-----+
a      L V A D L V N A Q K D S M Q D E S S Q T -
      -----+-----+-----+-----+-----+
1321      tcattacagaaagagattagtactgaagagcagctaaggcgctgcaagaggagaagctt 1380
      -----+-----+-----+-----+-----+
a      S L Q K E I S T E E Q L R R L Q E E K L -
      -----+-----+-----+-----+-----+
1381      tgcaaaaatctgtatggatagaaaatttgctatcgtttttgttcccttgtggacatctagtc 1440
      -----+-----+-----+-----+-----+
```

Fig. 1 (page 4 of 7)

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# HUMAN xiap

```

a      C K I C M D R N I A I V F V P C G H L V -
      actgtaaacaatgtgctgaagcagttgacaagtgcccatgtgctacacagtcattact 1500
      1441 -----+-----+-----+-----+-----+-----+-----+
a      T C K Q C A E A V D K C P M C Y T V I T -
      ttcaagcaaaaaattttatgtcttaacttaactctatagtaggcattgttatgtgttct 1560
      1501 -----+-----+-----+-----+-----+-----+-----+
a      F K Q K I F M S *
      tattaccctgattgaatgtgtgatgtgaactgactttaagtaatcaggattgaattcccat 1620
      1561 -----+-----+-----+-----+-----+-----+-----+
a      tagcatttgctaccaagtaggaaaaaaatgtacatggcagtggttttagttggcaatata 1680
      1621 -----+-----+-----+-----+-----+-----+-----+
a      atccttgaaatttcttgatttttcagggtattagctgtattatccattttttttactgtta 1740
      1681 -----+-----+-----+-----+-----+-----+-----+
a      tttaattgaaaccatagactaagaataagaagcatcataactataactgaacacaatgtgt 1800
      1741 -----+-----+-----+-----+-----+-----+-----+
a
  
```

Fig. 1 (page 5 of 7)

1801	attc	tagtatactgatttaatttctaagtgtaaagtgaaatcatctggatttttat	1860
a	-		-
1861	tcttttcagataggcttaacaaatggagcttcttgtatatataaatgtggagatttagagtta	1920	
a	-		-
1921	atctccccaatcacataaatttgttttgtgtgaaaaaggaataaaattgttccatgctggtg	1980	
a	-		-
1981	gaaagatagagattgttttagaggttggtgtgtgttttaggattctgtccattttct	2040	
a	-		-
2041	tgtaaagnnataaacacgnacntgtgcgaaatatntttgtaaagtgat ttgccattnttg	2100	
a	-		-
2101	aaagcgtaatttaatgataaatactatcgagccaacatgtactgacatggaaagatgtca	2160	
a	-		-

Fig. 1 (page 6 of 7)

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# HUMAN xiap

```

2161  nagatatgttaagtgtaaaatgcaagtggcnnnacactatgtatagtctgagccagatca 2220
      - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
a

2221  aagtatgtatgttnttaatatgcatagaacnanagatttggaagatatcaccaaaactg 2280
      - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
a

2281  ttaaatgtggtttctctcggggaggggggattgggggagggcccccagaggggttcta 2340
      - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
a

2341  naggggccttttcacttttcnacttttttcattttgttctgttcgnatttttataagtat 2400
      - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
a

2401  gtanacccnaagggttttatggnaaactaacatcagtaaacctaacccccgtgactatcct 2460
      - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
a

2461  gtncctctccctaggagctgtnntgtttccaccaccaccccttccctctgaacaaatgc 2520
      - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
a

2521  ctgagtgtctggggcactttn 2540
      - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
a

```

Fig. 1 (page 7 of 7)

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# HUMAN hiap-1

```
SEQ ID NO:5  
1 TCCTTGAGATGTATCAGTATAGGATTAGGATCTCCATGTTGGAAGTCTCTAAATGCATAGA 60  
- - - - -  
c  
61 AATGGAAATAATGGAAATTTTTCATTTTGGCTTTTCAGCCCTAGTATTAAACTGATAAAA 120  
- - - - -  
c  
121 GCAAGCCATGCACAAAACCTACCTCCCTAGAGAAAGGCTAGTCCCTTTTCTTCCCCATTC 180  
- - - - -  
c  
181 ATTCATTATGAACATAGTAAAAACAGCATATCTTATCAAAATTGATGAAAAGCGCCA 240  
- - - - -  
SEQ ID NO:6 c  
241 ACACGTTTGAACGAAATACGACTTGTCTGTAAGTGTACCGAATGTCTACGTATTCCA 300  
- - - - -  
c  
301 CTTTCCCTGCTGGGTTCTCTCAGAAAGGAGTCTTGTCTCGTGTCTTCTATTACA 360  
- - - - -  
c  
F P A G V P V S E R S L A R A G F Y Y T -
```

Fig. 2 (page 1 of 8)



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## HUMAN hiap-1

```

361      CTGGTGTGAATGACAAGGTCAAATGCTTCTGTGTGGCCTGATGCTGGATAACTGGAAA 420
      +-----+-----+-----+-----+-----+-----+
      G V N D K V K C C F C C G L M L D N W K R -

421      GAGGACAGTCCCTACTGAAAAAGCATAAAAAGTTGTATCCTAGCTGCAGATTCTGTTTCTCAGA 480
      +-----+-----+-----+-----+-----+-----+
      G D S P T E K K H K K L Y P S C R F V Q S -

481      GTCTAAATTCCGGTTAAACAACCTTGAAGCTACCTCTCAGCCTACTTTCTTCTTCAGTAA 540
      +-----+-----+-----+-----+-----+-----+
      L N S V N N L E A T S Q P T F P S S V T -

541      CACATTCCACACACTCATTACTTCCGGGTACAGAAACAGTGGATATTCCGTGGCTCTT 600
      +-----+-----+-----+-----+-----+-----+
      H S T H S L L P G T E N S G Y F R G S Y -

601      ATTCAACTCTCCATCAAATCCTGTAAACTCCAGAGCAAATCAAGAATTTCTGCTTGA 660
      +-----+-----+-----+-----+-----+-----+
      S N S P S N P V N S R A N Q E F S A L M -

661      TGAGAAAGTTCCCTACCCCTGTCCAATGAATAACGAAATGCCAGATTACTTACTTTTCAGA 720
      +-----+-----+-----+-----+-----+-----+
      R S S Y P C P M N N E N A R L L T F Q T -

```

Fig. 2 (page 2 of 8)

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## HUMAN hiap-1

```

721 CATGGCCATTGACTTTTCTGTGCGCCAACAGATCTGGCACGAGCAGGCTTTTACTACATAG 780
      W P L T F L S P T D L A R A G F Y Y I G -
781 GACCTGGAGACAGAGTGGCTTGCTTGGCTGTGGTGGAATAATTGAGCAATTGGGAACCGA 840
      P G D R V A C F A C G G K L S N W E P K -
841 AGGATAATGCTATGTCAGAACACCTGAGACATTTCCCAAATGCCCATTTATAGAAAATC 900
      D N A M S E H L R H F P K C P F I E N Q -
901 AGCTTCAAGACACTTCAAGATACACAGTTTCTAATCTGAGCATGCAGACACATGCAGCCCC 960
      L Q D T S R Y T V S N L S M Q T H A A R -
961 GCTTTAAACATTCCTTAACTGGCCCTCTAGTGTCTAGTTAATCCTGAGCAGCTTGCAA 1020
      F K T F F N W P S S V L V N P E Q L A S -
1021 GTGCGGGTTTTTATTATGTGGGTAACAGTGATGATGTCAAAATGCTTTTGTGTGATGGTG 1080
      A G F Y Y V G N S D D V K C C F C C D G G -
```

Fig. 2 (page 3 of 8)

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## HUMAN hiap-1

```
1081 GACTCAGGTGTTGGGAATCTGGAGATGATCCATGGGTTCAACATGCCAAGTGGTTTCCAA 1140
-----+-----+-----+-----+-----+-----+-----+
C L R C W E S G D D P W V Q H A K W F P R -

1141 GGTGTGAGTACTTGATAAGAAATTAAGGACAGGAGTTTCATCCGTCAAGTTCAAGCCAGTT 1200
-----+-----+-----+-----+-----+-----+-----+
C E Y L I R I K G Q E F I R Q V Q A S Y -

1201 ACCCTCATCTACTTGAACAGCTGCTATCCACATCAGACAGCCAGGAGATGAAAATGCAG 1260
-----+-----+-----+-----+-----+-----+-----+
C P H L L E Q L L S T S D S P G D E N A E -

1261 AGTCATCAATTATCCATTGGAACTGGAGAAGACCATTTCAGAAAGATGCAATCATGATGA 1320
-----+-----+-----+-----+-----+-----+-----+
C S S I I H L E P G E D H S E D A I M M N -

1321 ATACTCCTGTGATTAATGCTGCCGTGGAAATGGGCTTTAGTAGAAGCCTGGTAAACAGA 1380
-----+-----+-----+-----+-----+-----+-----+
C T P V I N A A V E M G F S R S L V K Q T -

1381 CAGTTCAGAGAAAAATCCTAGCAACTGGAGAGAAATTATAGACTAGTCAATGATCTTGTGT 1440
-----+-----+-----+-----+-----+-----+-----+
C V Q R K I L A T G E N Y R L V N D L V L -
```

Fig. 2 (page 4 of 8)

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## HUMAN hiap-1

```
1441 TAGACTTACTCAATGCAGAAGATGAAATAAGGGAAGAGGAGAGAGAAAGAGCAACTGAGG 1500
      D L L N A E D E I R E E E R A T E E -
1501 AAAAAGAATCAAATGATTATTATTAAATCCGGAAGAAATAGAAATGCCACTTTTCAACATT 1560
      K E S N D L L L I R K N R M A L F Q H L -
1561 TGACTTGTGTAATCCAATCCTGGATAGTCTACTAACTGCCGGAATTATTAAATGAACAAG 1620
      T C V I P I L D S L L T A G I I N E Q E -
1621 AACATGATGTTATAACAGAAGACACAGACGCTCTTACAAGCAAGAACTGATTGATA 1680
      H D V I K Q K T Q T S L Q A R E L I D T -
1681 CGATTTTAGTAAAGGAAATATTGCAGCCACTGTATTTCAGAAACTCTCTGCAAGAAGCTG 1740
      I L V K G N I A A T V F R N S L Q E A E -
1741 AAGTGTGTATATGAGCATTTATTGTGCAACAGCACATAAAATATATCCACAGAAG 1800
      A V L Y E H L F V Q Q D I K Y I P T E D -
```

Fig. 2 (page 5 of 8)

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## HUMAN hiap-1

```
1801 ATGTTTCAGATCTACCAAGTGAAGAACAAATTGCGGAGACTACCAGAAAGAAACATGTA 1860
-----+-----+-----+-----+-----+-----+-----+
      V S D L P V E E Q L R R L P E E R T C K -
1861 AAGTGTGTATGGACAAAGAGTGTCATAGTGTTTATTCCTTGGTGCATCTAGTAGTAT 1920
-----+-----+-----+-----+-----+-----+-----+
      V C M D K E V S I V F I P C G H L V V C -
1921 GCAAAGATTGTGCTCCTTCTTTAAGAAAGTGTCCTATTTGTAGGAGTACAATCAAGGTA 1980
-----+-----+-----+-----+-----+-----+-----+
      K D C A P S L R K C P I C R S T I K G T -
1981 CAGTTCGTACATTTCTTTCATGAAGAAGAACCAACATCGTCTAACTTTAGAATTAAAT 2040
-----+-----+-----+-----+-----+-----+-----+
      V R T F L S *
2041 TTATTAAATGTATTATAACTTTAACTTTTATCCTAATTTGGTTTCCTTAAATTTTATT 2100
-----+-----+-----+-----+-----+-----+-----+
      TATTACAAC TCAAAAACATTTGTTTGTGTAAACATATTTATATATGTATCTAAACCATA 2160
-----+-----+-----+-----+-----+-----+-----+
      -
      -
```

Fig. 2 (page 6 of 8)

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# HUMAN hiap-1

```
2161 TGAACATATATTTTGTAGAACTAAGAGAAATGATAGGCTTTTGTCTTATGAACGAAAAA 2220
-----+-----+-----+-----+-----+-----+-----+
c -

2221 GAGGTAGCACTACAAACACAATAATTCAATCCAAATTCAGCATTATTGAAATTGTAAGTG 2280
-----+-----+-----+-----+-----+-----+-----+
c -

2281 AAGTAAAACTTAAGATATTTGAGTTAACCTTTAAGAAATTTTAAATATTTTGCAATTGTAC 2340
-----+-----+-----+-----+-----+-----+-----+
c -

2341 TAATACCGGGAACATGAAGCCAGGTGTGGTGTATGTACCTGTAGTCCCAGGCTGAGGCA 2400
-----+-----+-----+-----+-----+-----+-----+
c -

2401 AGAGAAATTACTTGAGCCCAGGAGTTTGAATCCATCCTGGGCAGCATACTGAGACCCCTGCC 2460
-----+-----+-----+-----+-----+-----+-----+
c -

2461 TTATAAAACXAAACAGXACCAXCCAAACACCCAGGACACATTCTCTGCTTTTGTAT 2520
-----+-----+-----+-----+-----+-----+-----+
c -
```

Fig. 2 (page 7 of 8)

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# HUMAN hiap-1

```
2521 CAGTGTCCCTATACATCGAAGGTGTGCATATATGTTGAATCACATTTTAGGGACATGGTGT 2580
      - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
c

2581 TTTTATAAAGAAATTCGTGAGXAAAAATTTAATAAGCAACCCXAAATTACTCTTAAAAAA 2640
      - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
c

2641 AAAAAAAAAAAAACTCGAGGGGCCCGTACCAAT 2676
      - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
c
```

Fig. 2 (page 8 of 8)

SEQ ID NO: 7

[illegible]

TAATTCAGAGAGATACTCATCCTACCTGAAATATAAATCCAGATAAAGAAAG  
-----+-----+-----+-----+-----+-----+  
61

121 TGAGTAAATTCTACATAAGAGCTATCATTTGATTTCTTTTGTGGTGGAAATCTTAGTT  
-----+-----+-----+-----+-----+-----+ 180

181 CATGTGAAGAAAATTTCAATGTGAATGTTTATAGCTATCAAAACAGTACTGTCACTACTCATG  
 240 - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +

CACAAAACTGCCCTCCCAAGACTTTTCCAGGTCCTCGTATCAAAACATTAAGAGTATA  
 -----+-----+-----+-----+-----+-----+-----+  
 241

**SEQ ID NO: 8 a**

ATGGAAGATAGCACGATCTTGTCTAGATTGGACAAACAGCAACAAACAAAATGAAGTAT  
 -----+-----+-----+-----+-----+-----+-----+  
 301 360

M E D S T I L S D W T N S N K O K M K Y -

Fig. 3 (page 1 of 7)



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## HUMAN hiap-2

```
361      GACTTTTCCTGTGAACCTACAGAATGTCTACATATTCAACTTCCCCCGGGGTCCT      420
      -----+-----+-----+-----+-----+-----+-----+
      D F S C E L Y R M S T Y S T F P A G V P -
      a

421      GTCTCAGAAAGGAGCTTGTCTCGTGTGGTTTATTATATACTGGTGTGAATGACAAGTCT      480
      -----+-----+-----+-----+-----+-----+-----+
      V S E R S L A R A G F Y Y T G V N D K V -
      a

481      AAATGCTTCTGTGGCCTGATGCTGGATAACTGGAACTAGGAGACAGTCCATTATCAA      540
      -----+-----+-----+-----+-----+-----+-----+
      K C F C C G L M L D N W K L G D S P I Q -
      a

541      AAGCATAAACAGCTATATCCTAGCTGTAGCTTTATTTCAGAACTGTTTCAGCTAGTCTG      600
      -----+-----+-----+-----+-----+-----+-----+
      K H K Q L Y P S C S F I Q N L V S A S L -
      a

601      GGATCCACCTCTAAGAATACGTCTCCAATGAGAAACAGTTTGCACATTCAATATCTCCC      660
      -----+-----+-----+-----+-----+-----+-----+
      G S T S K N T S P M R N S F A H S L S P -
      a

661      ACCTTGGAACATAGTAGCTTGTTCAGTGGTTCTTACTCCAGCCTTCCTCCAAACCCTCTT      720
      -----+-----+-----+-----+-----+-----+-----+
      T L E H S S L F S G S Y S S L P P N P L -
      a
```

Fig. 3 (page 2 of 7)

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## HUMAN hiap-2

```

721  AATTCTAGAGCAGTTGAAGACATCTCTTCATCGAGGACTAACCCCTACAGTTATGCAATG
-----+-----+-----+-----+-----+-----+-----+
a    N S R A V E D I S S S R T N P Y S Y A M -
780  -

781  AGTACTGAAGAAGCCAGATTCTTACCTACCATATGTGGCCATTAACTTTTGTCAACCA
-----+-----+-----+-----+-----+-----+-----+
a    S T E E A R F L T Y H M W P L T F L S P -
840  -

841  TCAGAAATTGGCAAGAGCTGGTTTTTATTATATAGGACCTGGAGATAGGCTAGCCTGCTTT
-----+-----+-----+-----+-----+-----+-----+
a    S E L A R A G F Y Y I G P G D R V A C F -
900  -

901  GCCTGTGTGGGAAGCTCAGTAACTGGGAACCAAGGATGATGCTATGTCAGAACACCGG
-----+-----+-----+-----+-----+-----+-----+
a    A C G G K L S N W E P K D D A M S E H R -
1020  -

961  AGGCATTTTCCCAACTGTCCATTTTGGAAAAATCTCTAGAAAACCTCTGAGGTTAGCATT
-----+-----+-----+-----+-----+-----+-----+
a    R H F P N C P F L E N S L E T L R F S I -
1080  -

1021  TCAAATCTGAGCATGCAGACACATGCAGCTCGAATGAGAACAATTTATGTACTGGCCATCT
-----+-----+-----+-----+-----+-----+-----+
a    S N L S M Q T H A A R M R T F M Y W P S -
```

Fig. 3 (page 3 of 7)

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## HUMAN hiap-2

```
1081 AGTGTTCAGTTCAGCCTGAGCAGCTTGCAAGTCTGGTTTATTATGTGGTGGCAAT 1140
      S V P V Q P E Q L A S A G F Y Y V G R N -
1141 GATGATGTCAAATGCTTTGGTTGTGATGGTGGCTTGAGGTGTTGGGAATCTGGAGATGAT 1200
      D D V K C F G C D G G L R C W E S G D D -
1201 CCATGGGTAGAACATGCCAAGTGGTTTCCAAGGTGTGAGTCTTGATACGAATGAAAGGC 1260
      P W V E H A K W F P R C E F L I R M K G -
1261 CAAGAGTTTGTGATGAGATTCAAGGTAGATATCCTCATCTTCTTGAACAGCTGTTGTCA 1320
      Q E F V D E I Q G R Y P H L L E Q L L S -
1321 ACTTCAGATACCACTGGAGAAGAAAATGCTGACCCACCAATTATTCATTTTGACCTGGA 1380
      T S D T T G E E N A D P P I I H F G P G -
1381 GAAAGTTCTTCAGAAGATGCTGTCATGATGAATACACCTGTGGTTAAATCTGCCCTTGAA 1440
      E S S S E D A V M M N T P V V K S A L E -
```

Fig. 3 (page 4 of 7)

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## HUMAN hiap-2

1441	ATGGGCTTTAATAGAGACCTGGTGAAACAAACAGTTCTAAGTAAATCCTGACAACTGGA	1500
a	M G F N R D L V K Q T V L S K I L T T G	-
1501	GAGAACTATAAAACAGTTAATGATATGTGTGACGACCTTCTTAATGCTGAAGATGAAAAA	1560
a	E N Y K T V N D I V S A L L N A E D E K	-
1561	AGAGAAAGAGGAGAGGAAAAACAAGCTGAAGAAATGGCATCAGATGATTGTCTAATTAAT	1620
a	R E E E K E K Q A E E M A S D D L S L I	-
1621	CGGAAGAACAGAAATGGCTCTCTTTCAACAATTGACATGTGTGCTTCCTATCCTGGATAAT	1680
a	R K N R M A L F Q Q L T C V L P I L D N	-
1681	CTTTTAAAGGCCAATGTAATTAATAAAACAGGAACATGATATTAATAACAAAAACACAG	1740
a	L L K A N V I N K Q E H D I I K Q K T Q	-
1741	ATACCTTTACAAGCGAGAGAACTGATTGATACCATTGGGTTAAAGGAAATGCTGCGGCC	1800
a	I P L Q A R E L I D T I W V K G N A A A	-

Fig. 3 (page 5 of 7)

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## HUMAN hiap-2

```
1801 AACATCTTCAAAACTGTCTAAAGAAATTGACTCTACATTGTATAAGAACTTATTGTG 1860
      N I F K N C L K E I D S T L Y K N L F V -
1861 GATAAGAAATGAAGTATATCCAACAGAAAGATGTTTCAGGCTGTGTCACCTGGAAGACAA 1920
      D K N M K Y I P T E D V S G L S L E E Q -
1921 TTGAGGAGGTTGCAAGAAGAACGAACTTGTAAGTGTTGATGGACAAAGATTCTGTGTT 1980
      L R R L Q E E R T C K V C M D K E V S V -
1981 GTATTATTCCCTTGTTGTCATCTGGTAGTATGCCAGGAATGTGCCCTTCTCTAAGAAAA 2040
      V F I P C G H L V V C Q E C A P S L R K -
2041 TGCCCTATTTGCAGGGGTATAATCAAGGGTACTGTTCGTACATTCTCTCTTAAAGAAAA 2100
      C P I C R G I I K G T V R T F L S * -
2101 ATAGTCTATATTTAACTGCATAAAAAGGCTTTAAAAATATTGTTGAACACTTGAAGCC 2160
      a
```

Fig. 3 (page 6 of 7)

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## HUMAN hiap-2

```
2161  ATCTAAGTAAAAAGGAATTATGAGTTTTC AATTAGTAACATTCATGTTCTAGTCTGC 2220
      -----+-----+-----+-----+-----+-----+-----+
2221  TTTGGTACTAATAATCTTGTTTCTGAAAAGATGGTATCATATATTAAATCTTAATCTGTT 2280
      -----+-----+-----+-----+-----+-----+-----+
      -
2281  TATTTACAAGGGAAGATTTATGTTTGGTGAACTATATTAGTATGTATGTGTACCTAAGGG 2340
      -----+-----+-----+-----+-----+-----+-----+
      -
2341  AGTAGCGTCXCTGCTTGTTATGCATCATTTTCAGGAGTTACTGGATTGTGTTGTTCTTTTCAG 2400
      -----+-----+-----+-----+-----+-----+-----+
      -
2401  AAAGCTTTGAAXACTAAATTATAGTGTAGAAAAGAACTGGAAACCAGGAACCTCGGAGTT 2460
      -----+-----+-----+-----+-----+-----+-----+
      -
2461  CATCAGAGTTATGGTGCCGAATTGTCTTTGGTGCTTTTCACTTGTTGTTTAAAAATAAGGA 2520
      -----+-----+-----+-----+-----+-----+-----+
      -
2521  TTTTCTCTTATTTCTCCCCCTAGTTTGTGAGAAACATCTCAATAAAGTGCTTTAAAAAAG 2580
      -----+-----+-----+-----+-----+-----+-----+
      -
```

a

a

a

a

a

a

a

Fig. 3 (page 7 of 7)

23/61

# MOUSE xiap

```
SEQ ID NO:9      1      GACACTCTGCTGGCGGCGGCCCTCCTCCGGGACCTCCCTCGGGAACCGTCGCCCC 60
                  -
                  a
                  61      GCGGCGCTTAGTACTGGAGTGCTTGGCGGGAAGGTGGACAAGTCCTATTTTCCA 120
                  -
                  a
                  121      GAGAAGATGACTTTTAACAGTTTGAAGGAAGTCTTTGTACTTGCAGACACCAAT 180
                  -
                  M T F N S F E G T R T F V L A D T N -
                  181      AAGGATGAAGAATTGTAGAAGAGTTAATAGATTAAAAACATTTGCTAACTTCCCAAGT 240
                  -
                  K D E E F V E E F N R L K T F A N F P S -
                  a
                  241      AGTAGTCCTGTTTCAGCATCAACATTTGGCGGAGCTGGGTTTCTTTATACCGTGAAGGA 300
                  -
                  S S P V S A S T L A R A G F L Y T G E G -
                  a
                  301      GACACCGTGCAATGTTTCAGTTGTATGCGGCAATAGATAGATGGCAGTATGGAGACTCA 360
                  -
                  D T V Q C F S C H A A I D R W Q Y G D S -
                  a
```

Fig. 4 (page 1 of 6)

24/61

# MOUSE xiap

```
361      GCTGTTGGAAGACACAGGAGAAATATCCCCAAATTGCAGATTATCAATGGTTTATTTT 420
-----+-----+-----+-----+-----+-----+-----+-----+
a      A V G R H R R I S P N C R F I N G F Y F -

421      GAAAATGGTGTGCACAGTCTACAAATCCTGGTATCCAAAATGGCCAGTACAAATCTGAA 480
-----+-----+-----+-----+-----+-----+-----+-----+
a      E N G A A Q S T N P G I Q N G Q Y K S E -

481      AACTGTGTGGGAAATAGAAATCCTTTTGCCCTTGACAGGCCACCTGAGACTCATGCTGAT 540
-----+-----+-----+-----+-----+-----+-----+-----+
a      N C V G N R N P F A P D R P P E T H A D -

541      TATCTCTGAGAACTGGACAGGTGTAGATATTTCAGACACCATATACCCGAGGAACCCT 600
-----+-----+-----+-----+-----+-----+-----+-----+
a      Y L L R T G Q V V D I S D T I Y P R N P -

601      GCCATGTGTAGTGAAGAAGCCAGATTGAAGTCATTTCAGAACTGGCCGGACTATGCTCAT 660
-----+-----+-----+-----+-----+-----+-----+-----+
a      A M C S E E A R L K S F Q N W P D Y A H -

661      TTAACCCCCAGAGAGTTAGTGTAGTGTGGCTCTACTACACAGGGGCTGATCAAGTG 720
-----+-----+-----+-----+-----+-----+-----+-----+
a      L T P R E L A S A G L Y Y T G A D D Q V -
```

Fig. 4 (page 2 of 6)



25/61

# MOUSE xiap

```

721  CAATGCTTTTGTGGGGAAACTGAAAAATTGGGAACCCCTGTGATCGTGCCTGGTCA 780
      Q C F C C G G K L K N W E P C D R A W S -
841  GAACACAGGAGACACTTCCCAATTGCTTTTGTGTTTGGCCGGAACGTTAATGTTTCA 840
      E H R R H F P N C F F V L G R N V N V R -
901  AGTGAATCTGGTGTGAGTCTGATAGGAATTCCCAAAATCAACAACTCTCCAAGAAAT 900
      S E S G V S S D R N F P N S T N S P R N -
961  CCAGCCATGGCAGAATATGAAGCACGGATCGTTACTTTTGGAAACATGGATATACTCAGTT 960
      P A M A E Y E A R I V T F G T W I Y S V -
1021 AACAAAGGAGCAGCTTGCAAGAGCTGGATTTTATGCTTTAGGTGAAGCGGATAAAGTGAAG 1020
      N K E Q L A R A G F Y A L G E G D K V K -
      TGCTTCCACTGTGGAGGAGGCTCACGGATTGGAAGCCAAGTGAAGACCCCTGGGACCAG 1080
      C F H C G G G L T D W K P S E D P W D Q -

```

Fig. 4 (page 3 of 6)

26/61

## MOUSE xiap

```
1081 CATGCTAAGTGCTACCCAGGTGCAAAATACCTATTGGATGAGAAGGGCAAGAATATATA 1140
      H A K C Y P G C K Y L L D E K G Q E Y I -
1141 AATAATATTCAATTAAACCCATCCACTTGAGGAATCTTTGGGAAGAACTGCTGAAAAACA 1200
      N N I H L T H P L E E S L G R T A E K T -
1201 CCACCGCTAACTAAAAAATCGATGATACCATCTTCCAGAAATCCTATGGTGCAAGAAGCT 1260
      P P L T K K I D D T I F Q N P M V Q E A -
1261 ATACGAATGGGATTAGCTTCAAGGACCTTAAGAAAAACAATGGAAGAAAAATCCAAACA 1320
      I R M G F S F K D L K K T M E E K I Q T -
1321 TCCGGGAGCAGCTATCTATCACTTGAGGTCCTGATTGCAGATCTTGTGAGTGCTCAGAAA 1380
      S G S S Y L S L E V L I A D L V S A Q K -
1381 GATAATACGGAGGATGAGTCAAGTCAAACTTCATTGCAGAAAGACATTAGTACTGAAGAG 1440
      D N T E D E S S Q T S L Q K D I S T E E -
```

Fig. 4 (page 4 of 6)

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MOUSE xiap

```
1441 CAGCTAAGGCGCCTACAAGAGGAGAGCTTTCCAAAATCTGTATGGATAGAAATATTGCT 1500
      Q L R R L Q E E K L S K I C M D R N I A -
1501 ATCGTTTTTTTCTGTGGACATCTGGCCACTTGTAAACAGTGTGCAGAACGAGTTGAC 1560
      I V F F P C G H L A T C K Q C A E A V D -
1561 AAATGTCCCATGTGCTACACCGTCATTACGTTCAACCAAAAATTTTATGCTTAGTGG 1620
      K C P M C Y T V I T F N Q K I F M S * -
1621 GGCACCACATGTTATGTTCTTCTTGCTCTAATTGAATGTGTAATGGGAGCGGAACCTTTAAG 1680
      TAATCCTGCATTTGCATTCCATTAGCATCCTGCTGTTTCCAAATGGAGACCAATGCTAAC 1740
      AGCACTGTTTCCGTCCTAAACATTCAATTCTCGATCTTTTCGAGTTATCAGCTGTATCATTT 1800
      a
```

Fig. 4 (page 5 of 6)

28/61

# MOUSE xiap

```

1801 TAGCCAGTGTGTTTACTCGATTGAAACCTTAGACAGAGAAGCATTTTATAGCTTTTCACAT 1860
      -
1861 GTATATTGGTAGTACACTGACTTGATTCTATATGTAAGTGAATTCATCACCTGCATGTT 1920
      -
1921 TCATGCCCTTTTGCATAAGCTTAACAAATGGAGTGTCTGTATAAGCATGGAGATGTGATG 1980
      -
1981 GAATCTGCCCAATGACTTTAATTGGCTTATTGTAAACACGGAAGAACTGCCCCACGCTG 2040
      -
2041 CTGGGAGGATAAAGATTGTTTTAGATGCTCAGTCTGTGTTTAGGATTCTGCCCATTTA 2100
      -
a
a
a
a

```

Fig. 4 (page 6 of 6)

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# M-hiap-1

SEQ ID NO:39	GAATTCGGGAGACCTACACCCCGGAGATCAGAGGTCAATTGCTGGCGTTCAGAGCCTAG	1	60
	GAAAGTGGGCTGCGGTATCAGCCCTAGCAGTAAACCGACCAGAGCCATGCACAAACTAC	61	120
	ATCCCCAGAGAAAGACTTGTCCCTTCCCTCCCTGTCACTCACCATGAACATGGTTCAA	121	180
SEQ ID NO:40			M N M V Q -
	GACAGCGCCTTTCTAGCCCAAGCTGATGAAGAGTGCTGACACCTTTGAGTTGAAGTATGAC	181	240
	D S A F L A K L M K S A D T F E L K Y D		-
	TTTTCCTGTGAGCTGTACCGATTGTCCACGATTTCAGCTTTTCCAGGGGAGTTCCTGTG	241	300
	F S C E L Y R L S T Y S A F D R G V P V		-
	TCAGAAAGGAGTCTGGCTCGTGGCTTTTACTACACTGGTGCCCAATGACAAGGTCAAG	301	360
	S E R S L A R A G F Y Y T G A N D K V K		-
	TGCTTCTGTGGCCTGATGCTAGACAACTGGAACAAGGGGACAGTCCCATGGAGAAG	361	420
	C F C C G L M L D N W K Q G D S P M E K		-

Fig. 5 (page 1 of 6)

421	CACAGAAAGTTGTACCCAGCTGCAACTTTGTACAGACTTTGAATCCAGCCAACAGTCTG	480
	H R K L Y P S C N F V Q T L N P A N S L	-
481	GAAGCTAGTCCTCGGCCTTCTCTTCCACGGCGATGAGCACCATGCCCTTTGAGCTTT	540
	E A S P R P S L P S T A M S T M P L S F	-
541	GCAAGTTCTGAGAAATACTGGCTATTTCAGTGGCTCTTACTCGAGCTTTCCTCAGACCCCT	600
	A S S E N T G Y F S G S Y S S F P S D P	-
601	GTGAACTTCCGAGCAAATCAAGATTGTCTCTGCTTTGAGCACAAAGTCCCTACCACTTTGCA	660
	V N F R A N Q D C P A L S T S P Y H F A	-
661	ATGAACACAGAGAAGGCCAGATTACTCACCTATGAAAACATGGCCATTGTCTTTCTGTCA	720
	M N T E K A R L L T Y E T W P L S F L S	-
721	CCAGCAAAGCTGGCCAAAGCAGGCTTCTACTACATAGGACCTGGAGATAGATGGCCTGC	780
	P A K L A K A G F Y Y I G P G D R V A C	-

Fig. 5 (page 2 of 6)

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# M-hiap-1

```

781 TTTGCGTGGGAACTGAGCAACTGGGAACGTAAGGATGATGCTATGTCAGAGCAC      840
    F A C D G K L S N W E R K D D A M S E H -
    CAGAGGCATTCCCCAGCTGTCCGTTCTTALLkGACTTGGGTCAGTCTGCTTCGAGATAC      900
    Q R H F P S C P F L K D L G Q S A S R Y -
    ACTGTCTCTAACCTGAGCATGCAGACACACGAGCCCGTATTAGAACATTCTCTAACTGG      960
    T V S N L S M Q T H A A R I R T F S N W -
    CCTTCTAGTGCACTAGTTCAATCCCAGGAACCTTGCAAGTGCGGGCTTTTATTATACAGGA      1020
    P S S A L V H S Q E L A S A G F Y Y T G -
    CACAGTGATGATGTCAAGTGTTTATGCTGTGATGGTGGGCTGAGGTGCTGGGAATCTGGA      1080
    H S D D V K C L C C D G G L R C W E S G -
    GATGACCCCTGGGTGGAACATGCCAAGTGGTTTCCAAGGTGTGAGTACTTGCTCAGAATC      1140
    D D P W V E H A K W F P R C E Y L L R I -
    AAAGGCCAAGAATTGTGAGCCCAAGTTCAAGCTGGCTATCCTCATCTACTTGAGCAGCTA      1200
    K G Q E F V S Q V Q A G Y P H L L E Q L -
  
```

Fig. 5 (page 3 of 6)

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# M-hiap-1

```

1201 TTATCTACGTCAGACTCCCCAGAAGATGAGAATGCAGACGCAGCAATCGTGCAATTTGGC
    L S T S D S P E D E N A D A A I V H F G -
1260

1321 CCTGGAGAAAGTTCGGAAGATGTCGTCATGATGAGCACGCCCTGTGGTTAAAGCAGCCTTG
    P G E S S E D V V M M S T P V V K A A L -
1380

1381 GAAATGGGCTTCAGTAGGAGCCCTGGTGAGACAGACGGTTTCAGTGGCAGATCCTGGCCACT
    E M G E S R S L V R Q T V Q W Q I L A T -
1440

1441 GGTGAGAACTACAGGACCGTCAGTGACCTCGTTATAGGCTTACTCGATGCAGAACGAG
    G E N Y R T V S D L V I G L L D A E D E -
1500

1501 ATGAGAGAGGAGCAGATGGAGCAGCGCGCGGAGGAGGAGTCAGATGATCTAGCACTA
    M R E E Q M E Q A A E E E S D D L A L -
1560

1561 ATCCGGAAGAACAAAATGGTGCTTTTCCAAACATTTCACGTGTGTGACACCAATGCTGTAT
    I R K N K M V L F Q Q H L T C V T P M L Y -

```

Fig. 5 (page 4 of 6)



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# M-hiap-1

```
1561 TGCCCTCCTAAGTCAAGGCCATCACTGAACAGGAGTGCAATGCTGTGAAACAGAAACCA 1620
      C L L S A R A I T E Q E C N A V K Q K P -
1621 CACACCTTACAAGCAAGCACACTGATTGATACTGTGTAGCAAAAGGAAACACTGCAGCA 1680
      H T L Q A S T L I D T V L A K G N T A A -
1681 ACCTCATTCAGAAACTCCCTTCGGGAAATTGACCCCTGCGTTATACAGAGATATATTGTG 1740
      T S F R N S L R E I D P A L Y R D I F V -
1741 CAACAGGACATTAGGAGTCTTCCACAGATGACATTGCAGCTCTACCAATGGAAGAACAG 1800
      Q Q D I R S L P T D D I A A L P M E E Q -
1801 TTGCGGCCCTCCCGGAGGACAGAATGTGTAAAGTGTGTATGGACCGAGAGGTATCCATC 1860
      L R P L P E D R M C K V C M D R E V S I -
1861 GTGTTTCATCCCTGTGGCCATCTGGTCGTGTGCAAAAGACTGCGCTCCCTCTCTGAGGAAG 1920
      V F I P C G H L V V C K D C A P S L R K -
```

Fig. 5 (page 5 of 6)

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# M-hiap-1

```

1921 TGTCCCATCTGTAGAGGGACCATCAAGGCACAGTGGGCACATTTCTCTCTGAACAAGA 1980
-----+-----+-----+-----+-----+-----+-----+
C P I C R G T I K G T V R T F L S *
-

1981 CTAATGGTCCATGGCTGCAACTTCAGCCAGGAGGAAGTTCACTGTCTCACTCCCAGTTCCAT 2040
-----+-----+-----+-----+-----+-----+-----+
TCGGAACTTGAGGCCAGCCTGGATAGCACGAGACACCGCCAAACKCACAAATATAAACAT
2041 -----+-----+-----+-----+-----+-----+-----+
GAAAACTTTTGTCTGAAGTCAAGAATGAATGAATTAATTATAATAATTTAATTGGT
2101 -----+-----+-----+-----+-----+-----+-----+
TTCCTTAAAGTGCTATTGTGTTCCCAACTCAGAAAATGTTTCTGTAAACATATTACA 2160
-----+-----+-----+-----+-----+-----+-----+
TACTACCTGCATCTAAAGTATTTCATATATTCATATATTCAGATGTCTGAGAGAGGGTTT 2220
-----+-----+-----+-----+-----+-----+-----+
TGTTCTTGTTCCTGAAAAGCTGGTTTATCATCTGTGATCAGCATATACGCGCAACGGGCAG 2280
-----+-----+-----+-----+-----+-----+-----+
GGCTAGAATCCATGAACCAAGCTGCAAGATCTCAGCTAAATAAGCGGAAAGATTGG 2340
-----+-----+-----+-----+-----+-----+-----+
AGAAACGAAAGGAAATTTCTTCCTGTCCCAATGTATACCTTTCAGACTAATGACCTCTTCC 2400
-----+-----+-----+-----+-----+-----+-----+
TATCAAGCCTTCTA
2461 -----+-----+-----+-----+-----+-----+-----+
2474

```

Fig. 5 (page 6 of 6)

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## M-hiap-2

```
SEQ ID NO:41      CTGTGGTGAGATCTATTGTCCAAGTGGTGAGAACTTCATCTGGAAGTTAAGCGGTCA
1  -----+-----+-----+-----+-----+-----+
   GAAATACTATTACTACTCATGGACAKRACTGTCTCCAGAGACTCGCCCAAGGTACCTTA
61 -----+-----+-----+-----+-----+-----+
   CACCCRAAAACTTAAACGTATAATGGAGAAGACACAATCTTGTCAAATTGGACAAAGGA
121 -----+-----+-----+-----+-----+-----+
                        M E K S T I L S N W T K E
SEQ ID NO:42      GAGCGAAGAAAAATGAAGTTTGACTTTTCGTGTGAACCTTACCGAATGTCTACATATTC
181 -----+-----+-----+-----+-----+-----+
   S E E K M K F D F S C E L Y R M S T Y S
241 -----+-----+-----+-----+-----+-----+
   AGCTTTTCCAGGGAGTTCCTGTCTCAGAGAGGAGTCTGGCTCGTGGCTTTTATTA
300 -----+-----+-----+-----+-----+-----+
   A F P R G V P V S E R S L A R A G F Y Y
360 -----+-----+-----+-----+-----+-----+
   TACAGGTGTGAATGACAAAGTCAAGTGCTTCTGTGTGGCCTGATGTTGGATAACTGGAA
361 -----+-----+-----+-----+-----+-----+
   T G V N D K V K C F C C G L M L D N W K
420 -----+-----+-----+-----+-----+-----+
   ACAAGGGACAGTCCGTGTGAAAAGCACAGACAGTTCATCCAGCTGCAGCTTGTACA
361 -----+-----+-----+-----+-----+-----+
   Q G D S P V E K H R Q F Y P S C S F V Q
```

Fig. 6 (page 1 of 6)

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## M-hiap-2

```

421  GACTCTGCTTTCAGCCAGTCTGCAGTCTCCATCTAAGAATATGTCTCCTGTGAAAAGTAG
      +-----+-----+-----+-----+-----+-----+
      T L L S A S L Q S P S K N M S P V K S R - 480
      -
481  ATTTGCACATTGTCACCTCTGGAAACGAGGTGGCATTCACTCCAACCTGTGCTCTAGCCC
      +-----+-----+-----+-----+-----+-----+
      F A H S S P L E R G G I H S N L C S S P - 540
      -
541  TCTTAATTCTAGACAGTGGAAGACTTCTCATCAAGGATGGATCCCTGCAGCTATGCCAT
      +-----+-----+-----+-----+-----+-----+
      L N S R A V E D F S S R M D P C S Y A M - 600
      -
601  GAGTACAGAAGAGGCCAGATTTCTTACTTACAGTATGTGGCCTTTAAGTTTCTGTCACC
      +-----+-----+-----+-----+-----+-----+
      S T E E A R F L T Y S M W P L S F L S P - 660
      -
661  AGCAGAGCTGGCCAGAGCTGGCTTCTATTACATAGGCCCTGGAGACAGGGTGGCCCTGTTT
      +-----+-----+-----+-----+-----+-----+
      A E L A R A G F Y Y I G P G D R V A C F - 720
      -
721  TGCCTGTGGTGGAAACTGAGCAACTGGGAACCAAGGATTATGCTATGTCAGAGCACCG
      +-----+-----+-----+-----+-----+-----+
      A C G G K L S N W E P K D Y A M S E H R - 780
      -
```

Fig. 6 (page 2 of 6)

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## M-hiap-2

```
781 CAGACATTTCCCACTGTCCATTCTGAAAATACTTCAGAAACACAGAGTTAGTAT +-----+ 840
    R H F P H C P F L E N T S E T Q R F S I -
841 ATCAAATCTAAGTATGCAGACACACTCTGCTCGATTGAGGACATTTCTGTACTGGCCACC +-----+ 900
    S N L S M Q T H S A R L R T F L Y W P P -
901 TAGTGTTCCTGTTCAGCCCAGCAGCTTGCAAGTGCTGGATTCTATTACGTGGATCGCRA +-----+ 960
    S V P V Q P E Q L A S A G F Y Y V D R N -
961 TGATGATGTCAAGTGCCTTTGTGTGATGGTGGCTTGAGATGTTGGGAACCTGGAGATGA +-----+ 1020
    D D V K C L C C D G G L R C W E P G D D -
1021 CCCCTGGATAGAACACGCCAAATGGTTTCCAAGGTGTGAGTCTTGATACGGATGAAGGG +-----+ 1080
    P W I E H A K W F P R C E F L I R M K G -
1081 TCAGGAGTTTGTGATGAGATTCAAGCTAGATAATCCTCATCTTCTTGACAGCTGTTGTC +-----+ 1140
    Q E F V D E I Q A R Y P H L L E Q L L S -
```

Fig. 6 (page 3 of 6)

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## M-hiap-2

```

1141 CACTTCAGACACCCAGGAGAAGAAATGCTGACCCCTACAGAGACAGTGGTGCATTTGG
      T S D T P G E E N A D P T E T V V H F G - 1200
1201 CCCTGGAGAAAGTTCGAAAGATGTCGTCATGATGAGCACGCCCTGTGGTTAAAGCAGCCTT
      P G E S S K D V V M M S T P V V K A A L - 1260
1261 GGAAATGGGCTTCAGTAGGAGCCTGGTGAGACAGACGGTTCAGCGGCAGATCCTGGCCAC
      E M G F S R S L V R Q T V Q R Q I L A T - 1320
1321 TGGTGAGAACTACAGGACCGTCAATGATATTGTCTCAGTACTTTTGAATGCTGAAGATGA
      G E N Y R T V N D I V S V L L N A E D E - 1380
1381 GAGAAGAGAAGAGGAGAAGAAAGACAGACTGAAGAGATGGCATCAGGTGACTTATCACT
      R R E E E K E R Q T E E M A S G D L S L - 1440
1441 GATTCGGAAGAATAGAAATGGCCCTCTTTCAACAGTTGACACATGTCTTCTCCTATCCTGGA
      I R K N R M A L E Q Q L T H V L P I L D - 1500

```

Fig. 6 (page 4 of 6)

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## M-hiap-2

```
1501 TAATCTTCTTGAGGCCAGTGTAATTACAAAACAGGAACATGATATTATTAGACAGAAAC + 1560
      N L L E A S V I T K Q E H D I I R Q K T -
1561 ACAGATACCCTTACAAGCAAGAGAGCTTATTGACACCGTTTGTAGTCAAGGAAATGCTGC + 1620
      Q I P L Q A R E L I D T V L V K G N A A -
1621 AGCCAAACATCTTCAAAAACTCTCTGAAGGGAATTGACTCCACGTTATATGAAAACTTATT + 1680
      A N I F K N S L K G I D S T L Y E N L F -
1681 TGTGAAAAGAATATGAAGTATATTCCAACAGAAGACGTTTCAGGCTTGTCATTGGAAGA + 1740
      V E K N M K Y I P T E D V S G L S L E E -
1741 GCAGTTGCGGAGATTACAAGAAGAACGAACTTGCAAGTGTGTATGGACAGAGAGTTTC + 1800
      Q L R R L Q E E R T C K V C M D R E V S -
1801 TATTGTGTTTCATTCCGTGTGGTCATCTAGTAGTCTGCCAGGAATGTGCCCCCTTCTCTAAG + 1860
      I V F I P C G H L V V C Q E C A P S L R -
```

Fig. 6 (page 5 of 6)

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## M-hiap-2

```

1861 GAAGTGCCCATCTGCAGGGGACAATCAAGGGGACTGTGCGCACATTTCTCTCATGAGT 1920
      K C P I C R G T I K G T V R T F L S * -
1921 GAAGATGGTCTGAAGATATTGTTGGACATCAGAAGCTGTCAGAACAAAGAATGAACCTAC 1980
      - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
      TGATTTCAGCTCTTCAGCAGGACATCTACTCTCTTTCAAGATTAGTAATCTTGCTTTAT 1980
1981 - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + 2040
      GAAGGTAGCATTTGTATATTAAAGCTTAGTCTGTTGCAAGGGAAGGTCATGCTGTTGAG 2040
2041 - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + 2100
      CTACAGGACTGTGTCTGTTCCAGAGCAGGAGTTGGGATGCTTGCTGTATGTCCTTCAGGA 2100
2101 - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + 2160
      CTTCTTGGGATTTGGGAATTTGGGAAAGCTTTGGAATCCAGTATGTGGAGCTCAGAAA 2160
2161 - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + 2220
      TCCTGGAACCAAGTACTCTGGTACTCAGTAGATAGGGTACCCTGTACTTCTTGGTGCTTT 2220
2221 - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + 2280
      TCCAGTCTGGGAAATAAGGAGGAATCTGCTGCTGGTAAATAATTGCTGGATGTGAGAAAT 2280
2281 - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + 2340
      AGATGAAAGTGTTCGGGTGGGGCGTGTCATCAGTGTAGTGTGTCAGGGATGTATGCAG 2340
2341 - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + 2400
      GCCAACAACACTGTGTAG
2401 - - - - - + - - - - - 2416
```

Fig. 6 (page 6 of 6)



# Alignment of BIR (Baculoviral IAP Repeats) Domains

**Baculovirus**  
 Cp\_iap  
 Op\_iap  
**Human**  
 xiap  
 hiap1, hiap2  
**Mouse**  
 m-xiap  
**Insect**  
 diap

Cydia pomonella  
 Orgyia pseudotsugata  
 IAP on X chromosome  
 two different human IAP genes  
 mouse homologue of human xiap gene  
 Drosophila IAP gene, not clearly a homologue of xiap or hiap

Fig. 7

**note on consensus:** The consensus line represents amino acids or very similar amino acids which are present in 14 of the 19 BIR sequences at each position.  
 Capitalized residues are those that are in the consensus sequence.

SEQ ID NO:11	Op_iap-1	kaarLgTYtn	WPvqf.l	leps	rMAasGFYY1	GrgDeVrCaf	CkveitnWvr	gDdpetdHkr	wapqCpFV	41/61
SEQ ID NO:14	Cp_iap-1	eevRLnTFek	WPvsf.l	lspe	tMAknGFYY1	GrsDeVrCaf	CkveimrWke	gEdpaadHkk	wapqCpFV	68
SEQ ID NO:15	diap-2	eanRLvTFkd	WPnnpn.i	lpq	aLAKAGFY1	nrlDhVkcVw	CngviakWek	nDnafeeHkr	ffPqCprV	
SEQ ID NO:16	m-xiap-1	efnRLkTFan	FPsspsvas	tLARAGFLYt	GegDtVqCFs	GegDtVqCFs	ChaaidrWqy	gDsavgrHrr	isPnCrFI	
SEQ ID NO:17	xiap-1	efnRLkTFan	FPsgspvas	tLARAGFLYt	GegDtVrCFs	GegDtVrCFs	ChaaavdrWqy	gDsavgrHrk	vsPnCrFI	
SEQ ID NO:18	hiap1-1	elyRMstYst	FPagvpvser	sLARAGFYt	GvndKvKCFc	GvndKvKCFc	CglmldnWkr	gDsptekHkk	lyPsCrFV	
SEQ ID NO:19	hiap2-1	elyRMstYst	FPagvpvser	sLARAGFYt	GvndKvKCFc	GvndKvKCFc	CglmldnWk1	gDspiQkHkq	lyPsCsFI	
SEQ ID NO:20	m-xiap-2	eearLksFqn	WPdyahltp	eLASAGLYt	GadDqVqCFc	GadDqVqCFc	CggklknWep	cDrawseHrr	hfpnCfFv	
SEQ ID NO:21	xiap-2	eearLksFqn	WPdyahltp	eLASAGLYt	GigDqVqCFc	GigDqVqCFc	CggklknWep	cDrawseHrr	hfpnCfFv	
SEQ ID NO:22	hiap1-2	enaRLlTFqt	WP.lflspt	dLARAGFYi	GpgDrVaCfa	GpgDrVaCfa	CggklknWep	kDnamseHlr	hfpkCpFI	
SEQ ID NO:23	hiap2-2	eearFlTYhm	WP.lflsps	eLARAGFYi	GpgDrVaCfa	GpgDrVaCfa	CggklknWep	kDdamseHrr	hfpnCpFI	
SEQ ID NO:24	m-xiap-3	yearIvTFgt	Wiyv..nke	qLARAGFYal	GegDkVkcFh	GegDkVkcFh	CgggltdWkp	sEdpwdqHak	cyPgCkYl	
SEQ ID NO:25	xiap-3	yearIvTFgt	Wiyv..nke	qLARAGFYal	GegDkVkcFh	GegDkVkcFh	CgggltdWkp	sEdpweqHak	wyPgCkYl	
SEQ ID NO:26	hiap1-3	haaRFkTFfn	WPssvlvnp	qLASAGFYv	GnsDdVkcFc	GnsDdVkcFc	CdggllrcWes	gDdpwvqHak	wfPrCeYl	
SEQ ID NO:27	hiap2-3	haaRMrtFmy	WPssvpvqpe	qLASAGFYv	GnsDdVkcFg	GnsDdVkcFg	CdggllrcWes	gDdpwveHak	wfPrCeF1	
SEQ ID NO:28	Op_iap-2	eearLrTFae	WPrglkqrpe	eLAeAGFFYt	GqgDktrCFc	GqgDktrCFc	CdggllkdWep	dDapwqHak	wydrCeYv	
SEQ ID NO:29	Cp_iap-2	eearVksFhn	WPrcmkqrpe	qMADAGFFYt	GygDntkCFy	GygDntkCFy	CdggllkdWep	eDvpweqHvr	widrCaYv	
SEQ ID NO:30	diap-3	vdaRLrTFtd	WPisniqpas	aLAAGLYYq	kigDqVrCFh	kigDqVrCFh	Cniglrswqk	eDepwieHak	wsPkCqFV	
SEQ ID NO:31	diap-1	esvRLaTFge	WPlnapvsae	dLvanGFF..	GtwmeaeCdf	GtwmeaeCdf	ChvridrWey	gDlvaerHrr	ssPiCsmv	
SEQ ID NO:2	Consensus	---RL-TF--	WP-----	-LA-AGFY-	G--D-V-CF-	G--D-V-CF-	C-----W--	-D-----H--	--P-C-FV	

Fig. 8 (page 1 of 5)

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151	cp-iap	.....	.....msD	lrl.....	200
	diap	esDnegsvv	dspscscpd	lrl.....	EEVRLnTF ekWPv.sfls
	m-xiap	ppEthadyll	rtggvDiSD	tiyprnp.am	EanRLvTF kdWpn.pnit
	xiap	psEthadyll	rtggvDiSD	tiyprnp.am	csEEARLksf qnWPdyahLt
	hiap1	anq.....	EfSa	lmrssypcpM	qnWPdyahLt
	hiap2	avE.....	DiSS	srtnpysyam	qtWP..ltfls
	consensus	--E-----	-----D-SD	-----M	hmWP..ltfls
					EEARL-TF --WP-----L-
201	cp-iap	PetMAknGFY	YlGrSDeVrC	afCkveimrW	250
	diap	PqaLakAGFY	YlnrldhVkc	vwCnGviakW	kekEdpaADH kkwapqCPfV
	m-xiap	PrELAsAGLY	YtGadDqVqC	FcCGGKLkNW	EknDnAfeEH krFFPqCPrV
	xiap	PrELAsAGLY	YtGigDqVqC	FcCGGKLkNW	EPcDrAwSEH rRHFPnCfFV
	hiap1	PtDLArAGFY	YiGpgDrVaC	FaCGGKLsNW	EPcDrAwSEH rRHFPnCfFV
	hiap2	PsELArAGFY	YiGpgDrVaC	FaCGGKLsNW	EPkDnAmSEH lRHFPkCPFI
	consensus	P-ELA-AGFY	Y-G--D-V-C	F-CGGKL-NW	EPkDdAmSEH rRHFPnCpFl
					EP-D-A-SEH -RHFP-CPfV
251	cp-iap	kgidvcgsiv	ttnnignttt	hdtiigPahP	BIR 3 300
	diap	qmgplie.fa	tgknldelgi	qpttl.PlrP	kyAheaARvk sFhnWPrCmk
	m-xiap	lgrnvnvrse	s.gvssdrnF	pnStnsPrNP	kyAcvdaRlr TftdWpiSnI
	xiap	lgrnlnirse	s.davssdrnF	pnStnlPrNP	aMAeyeARiv TFgtWiys..
	hiap1	.....	enqlqdtSry	tvS.....Nl	SMAdyeARif TFgtWiys..
	hiap2	.....	ensl.etlrf	sis.....Nl	SMqthaARfk TFinWPSSvI
	consensus	-----	-----F	-----P-NP	SMqthaARmr TFmyWPSSvp
					-MA--AR-- TF--WP-S--

Fig. 8 (page 2 of 5)

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BIR 3		301	350
cp-iap	qrPEQMAAG	FFYtGyGDnt	KCFyCdGGLk dWepeDvPWe QHvrWFdrCa
diap	qpasaLAqAG	LYYqkiGdqv	rCFhCniGLr sWqkeDEPwf eHAKWSPkCq
m-xiap	VnkeQLARAG	FYalGeGDkV	KCFhCgGGLt dWkpsEDPwD QHAKcYPgCk
xiap	VnkeQLARAG	FYalGeGDkV	KCFhCgGGLt dWkpsEDPwD QHAKWYPgCk
hiap1	VnpEQLASAG	FYVvGnsDdV	KCFcCdGGLr cWesgDDPwV QHAKWFFPrCe
hiap2	VqPEQLASAG	FYVvGRsDdV	KCFgCdGGLr cWesgDDPwV eHAKWFFPrCe
consensus	V--EQLA-AG	FYY-G-GD-V	KCF-C-GGL- -W---DDPW- QHAKWFFP-C-
cp-iap	YvqlvKGrDY	VqkVit	400
diap	FvllaKGpAY	VseVlatta	..... aptlq.....
m-xiap	YlldeKGQeY	InnIhlthp.	LeESlgrTae kt..... Ppltk
xiap	YllegKGQeY	InnIhlths.	LeEcLvrTte kt..... Psltr
hiap1	YlirirKGQeY	IrqVqasyph	LlEqLlTsD spgdenaess iihlePgedh
hiap2	FlirmKGQeF	VdeIggrypH	LlEqLlTsD ttgeenadpp iihfgPgess
consensus	Yl---KGQeY	-----L-E-L--T--	-----P-----
cp-iap	..acVLpge.	.....	450
diap	..adVLmdea	pakeAltLGi	dggvVrnaiq rKllssGcaF stldeLlhDi
m-xiap	kiDdtifqnP	mVqeAirMGF	sfkdIKktme eKIqtsGssY lslevLIaDL
xiap	riDdtifqnP	mVqeAirMGF	sfkdIKkime eKIgisGsnY kslevLVaDL
hiap1	seDaIMmntP	vInaAveMGF	srsLVKqtVq rKIlatGenY rlvndLVIDL
hiap2	seDaVMmntP	vVksAleMGF	nrdLVKqtVl sKilttGenY ktvndiVsal
consensus	--D-V----P	-V--A--MGF	-----VK----- -KI---G---Y -LV-DL

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cp-iap	451	500
diap	.....	.....
m-xiap	fddagagaal Evreppe	.....
xiap	vsAqkDnted E.....	.....
hiap1	vnAqkDsmqD E.....	.....
hiap2	lnAedEireE Ererateeke sndlllirkn rmalfqhltc vipildslit	.....
consensus	lnAedEkreE Ekekqaeema sddslirkn rmalfqqltc vlpildnllk	.....
	--A----- E-----	-----
cp-iap	501	550
diap	.....	.....
m-xiap	.....	.....
xiap	.....	.....
hiap1	.....	.....
hiap2	.....	.....
consensus	.....	.....

Fig. 8 (sheet 4 of 5)

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Ring Zinc Finger		600
cp-iap	...tki... ..	Ekep q veDskLCKIC yveEciVcFV
diap	sniskitdei	nlslEEenRq LkDarLCKVC LDeEVgVVfL
m-xiap	.....k	diStEEQLRR LqEEkLsKIC MDrnlaiIVff
xiap	.....k	eiStEEQLRR LqEEkLCKIC MDrnlaiIVfV
hiap1	lyehlfvqgd	ikyiptedvs dlpvEEQLRR LpEErtCKVC MDKEVsIVFI
hiap2	lyknlfdvkn	mkyiptedvs glslEEQLRR LqEErtCKVC MDKEVsVVFI
consensus	-----	--S-EEQLRR L-EE-LCK-C MD-EV--VF-
		635
cp-iap	PCGHvVaCak CAISVdKCPM CRkIVtsvlk	vyFS.
diap	PCGHLatCnq CAPSVanCPM CRadiKgfvr	tFLS*
m-xiap	PCGHLatCkq CAeaVdKCPM CytVItfnqk	iFMS*
xiap	PCGHLVtCkq CAeaVdKCPM CytVItfkqk	iFMS*
hiap1	PCGHLVvCkd CAPSlrKCPi CRstIkgtvr	tFLS*
hiap2	PCGHLVvCqe CAPSlrKCPi CRGIkgtvr	tFLS.
consensus	PCGHLV-C-- CA-SV-KCPM CR--I-----	-FLS-

Fig. 8 (sheet 5 of 5)

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## Alignment of RZF (Ring Zinc Finger) Domains

### Baculovirus

Cp\_iap  
 Op\_iap  
 Human

xiap  
 hiap1, hiap2

### Mouse

m-xiap

### Insect

diap

Cydia pomonella  
 Orgyia pseudotsugata

IAP on X chromosome  
 two different human IAP genes

mouse homologue of human xiap gene

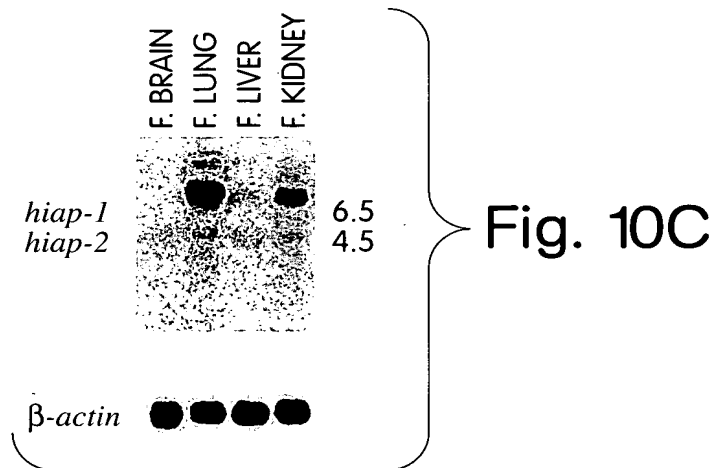
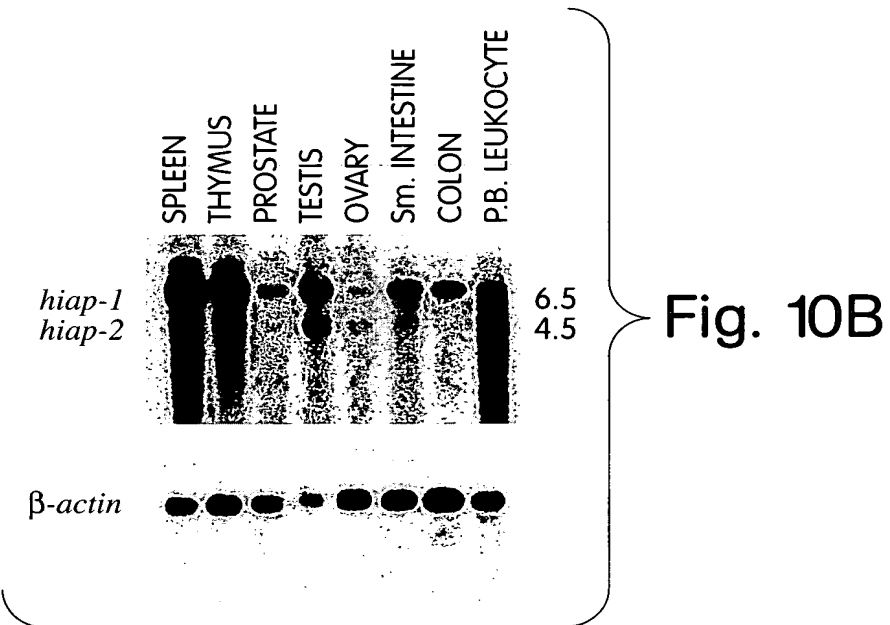
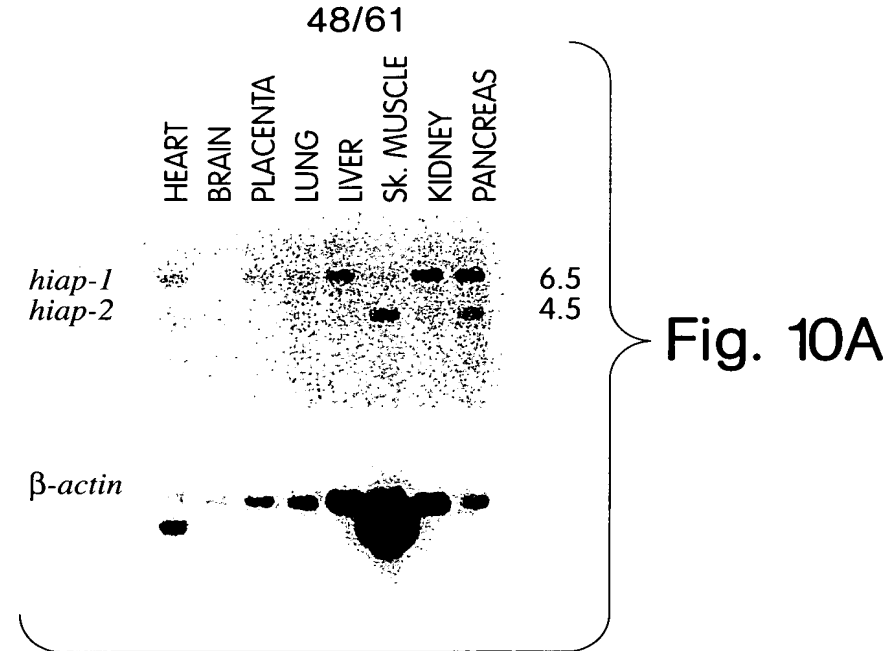
Drosophila IAP gene, not clearly a homologue of xiap or hiap

### note on consensus:

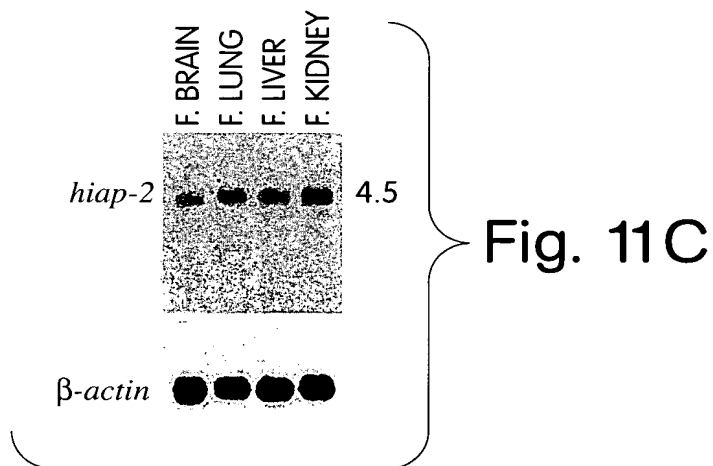
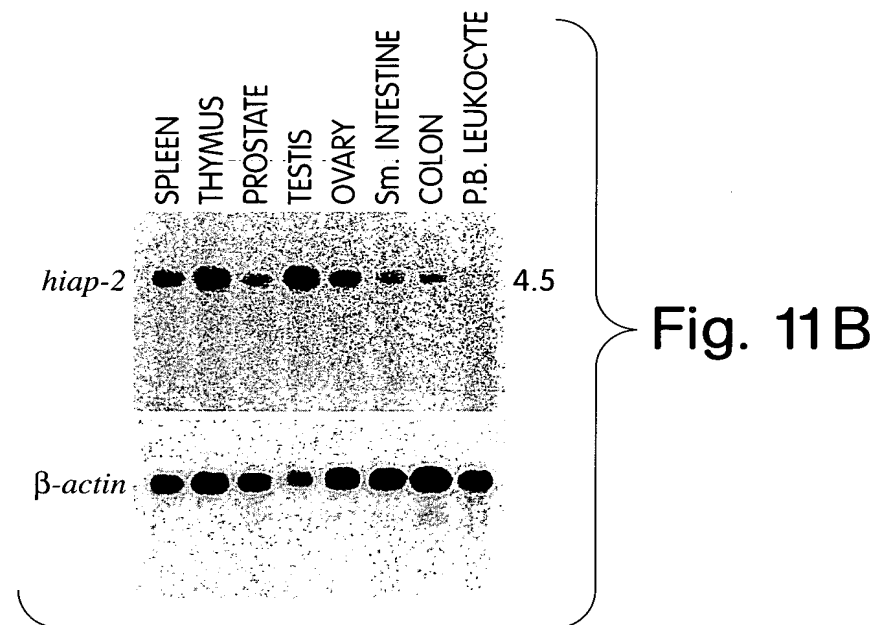
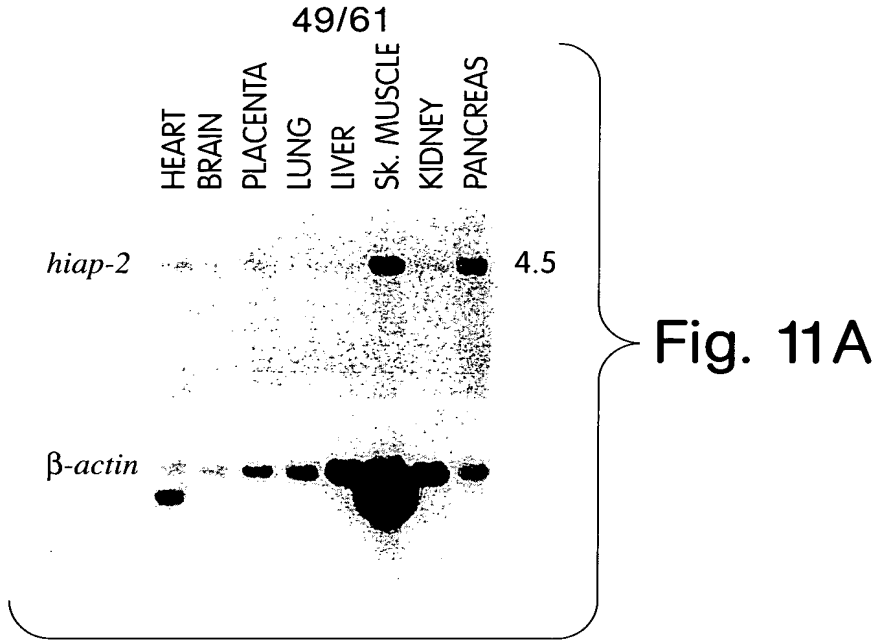
The consensus line represents amino acids or very similar amino acids which are present in 6 of the 7 RZF sequences at each position. Capitalized residues are those that are in the consensus sequence.

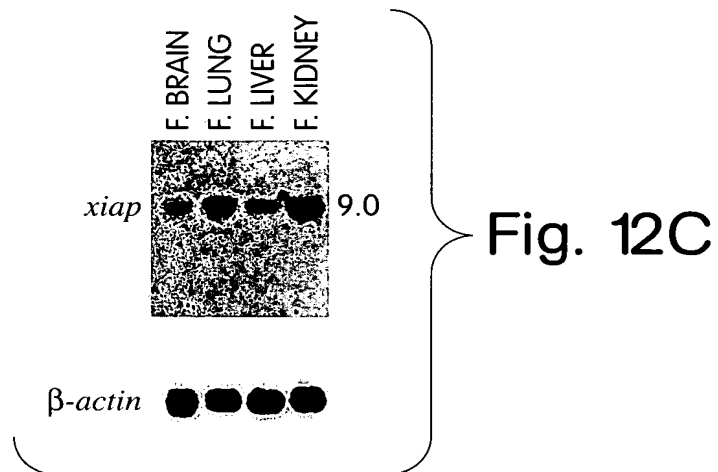
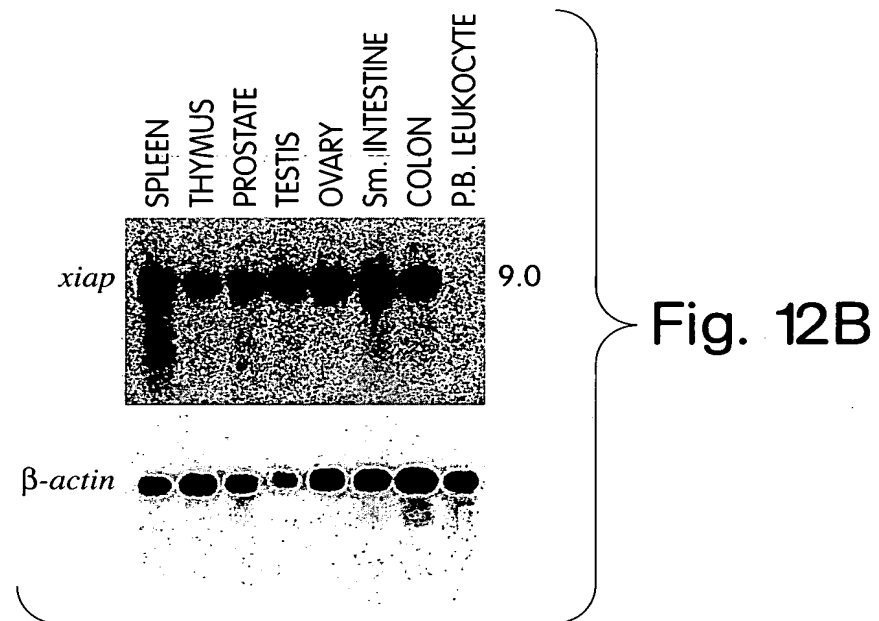
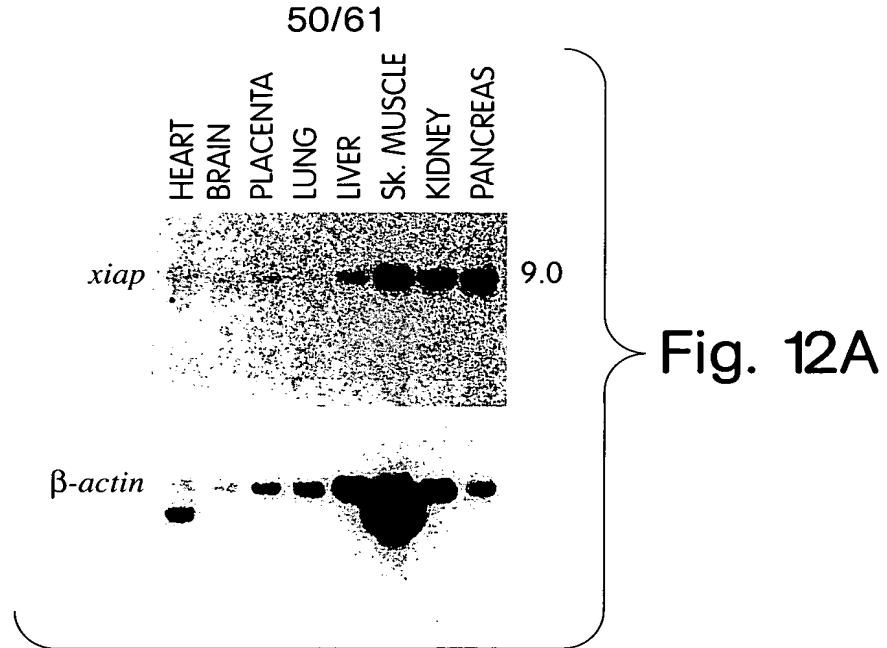
SEQ ID NO:32	hiap2	EqlrrlqEer	tCKVCMdkev	sVvFiPCGHl	vvCqeCApel	rkCPiC
SEQ ID NO:33	hiap1	EqlrrlpEer	tCKVCMdkev	sIVFiPCGHl	w CkdCAPsl	rkCPiC
SEQ ID NO:34	m-xiap	EqlrrlqEek	lSKICMdrni	aIVFfPCGHl	atCkqCAeav	dkCPmC
SEQ ID NO:35	xiap	EqlrrlqEek	lCKICMdrni	aIVFvPCGHl	vtCkqCAeav	dkCPmC
SEQ ID NO:36	diap	EenrqlkDar	lCKVCLdeev	gVvFlPCGHl	atCnqCApev	anCPmC
SEQ ID NO:37	Cp_iap	EkepgveDsk	lCKICyveec	iVcFvPCGHv	vaCakCAalsv	dkCPmC
SEQ ID NO:38	Op_iap	aveaevaDdr	lCKIClgack	tVcFvPCGHv	vaCgkCAagv	ttCPvC
SEQ ID NO:1	consensus	E-----E--	-CKICM----	-V-F-PCGH-	--C--CA----	--CP-C

Fig. 9









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S: STANDARDS	INCUBATION: OVERNIGHT											
	Hg			CEM-CM <sub>3</sub>			GT/CEM			JKT		
HIV	-	-	+	-	-	+	-	-	+	-	-	+
PHA/PMA	-	+	-	-	+	-	-	+	-	-	+	-
S	+	-	-	+	-	-	+	-	-	+	-	-

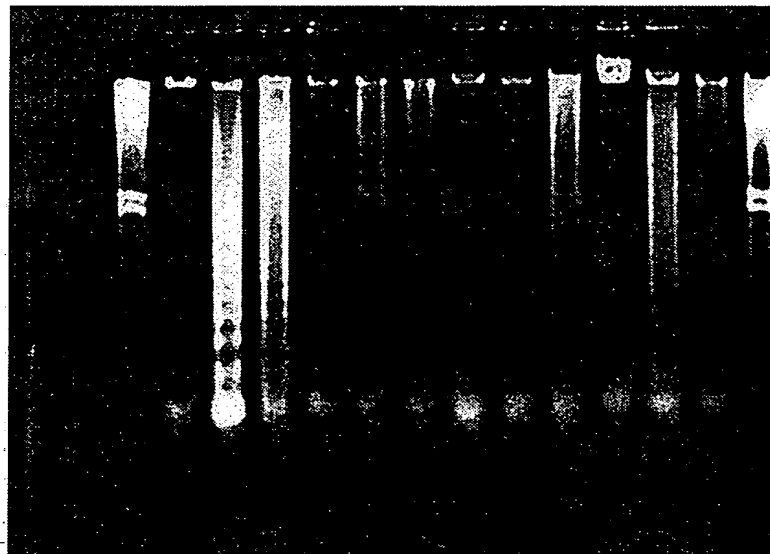


Fig. 13A

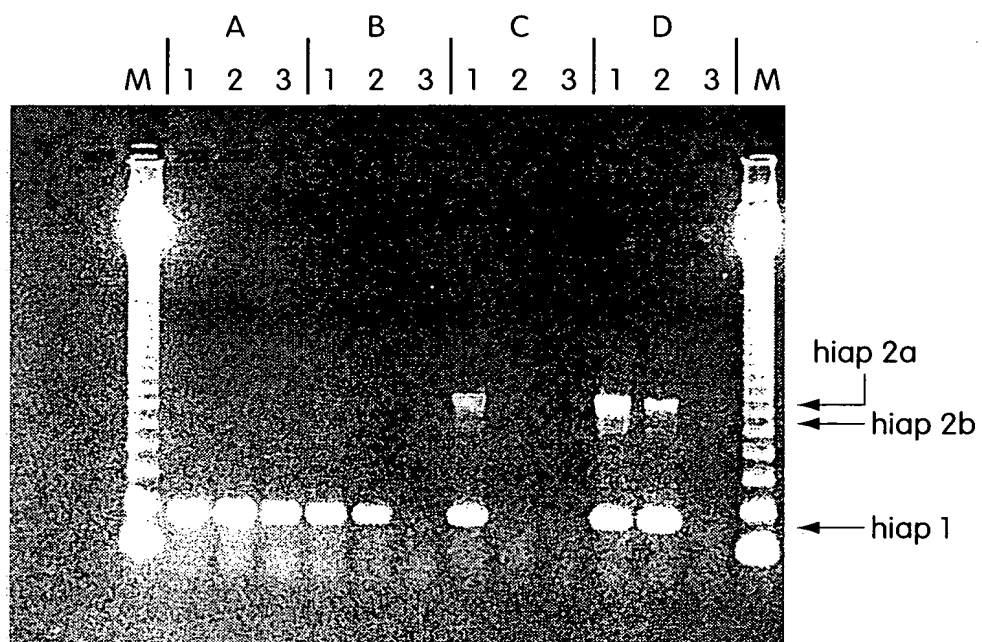


Fig. 13B

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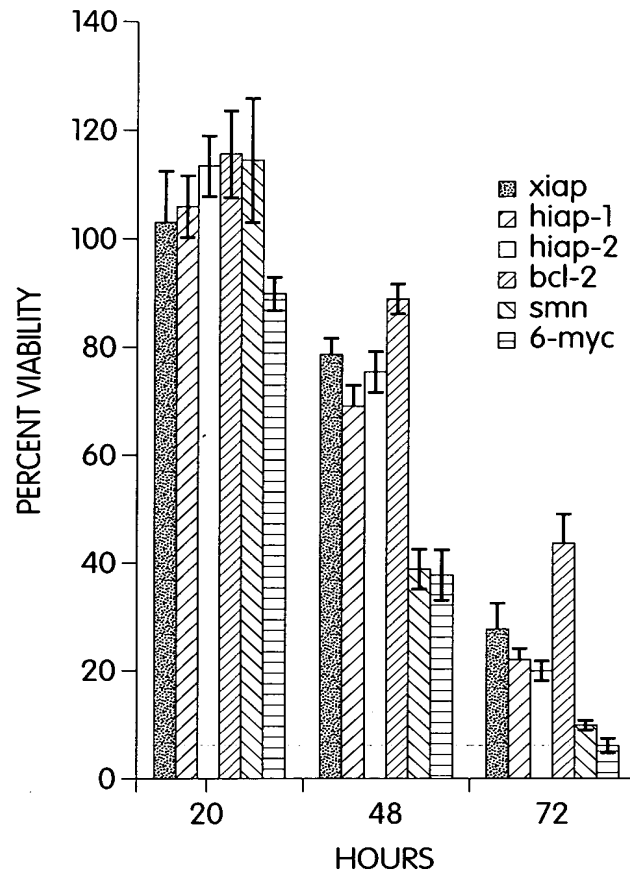


Fig. 14A

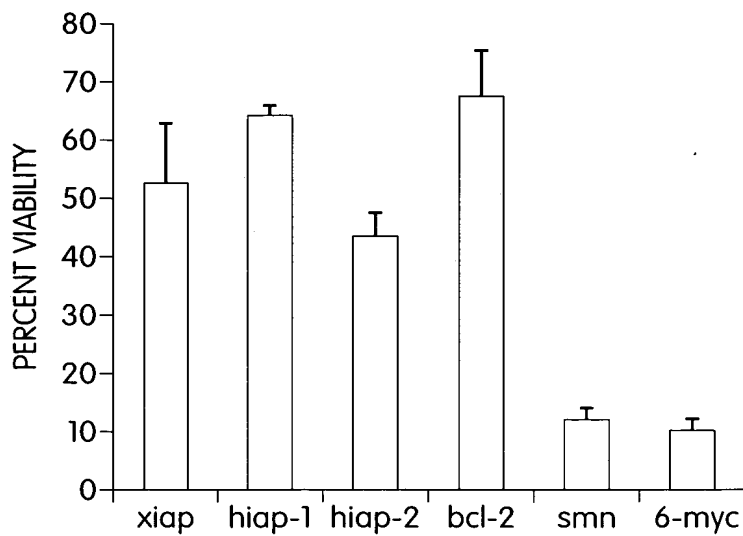


Fig. 14B

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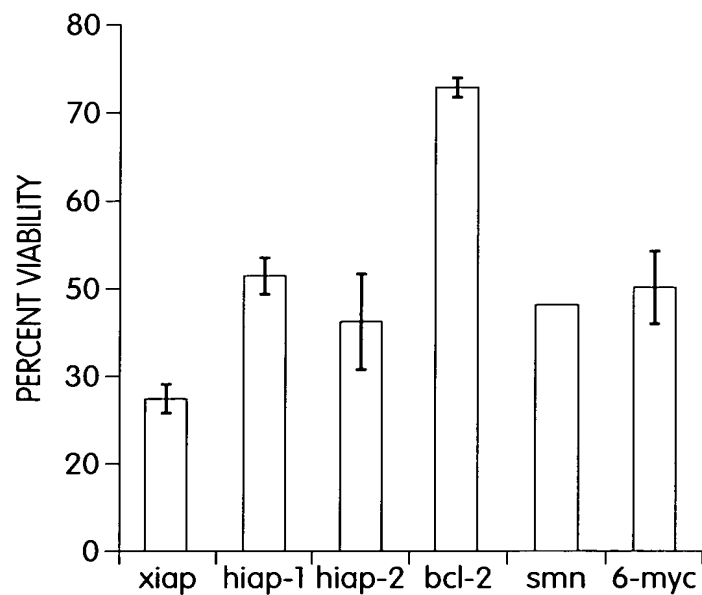


Fig. 14C

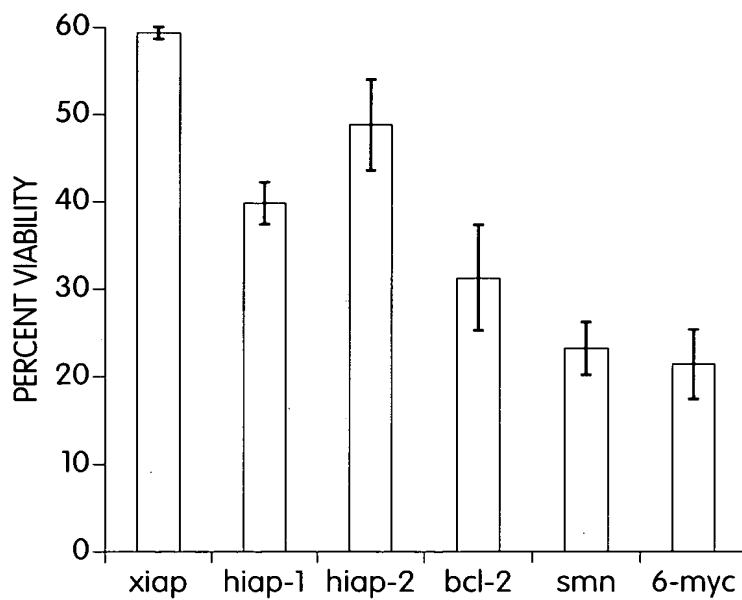
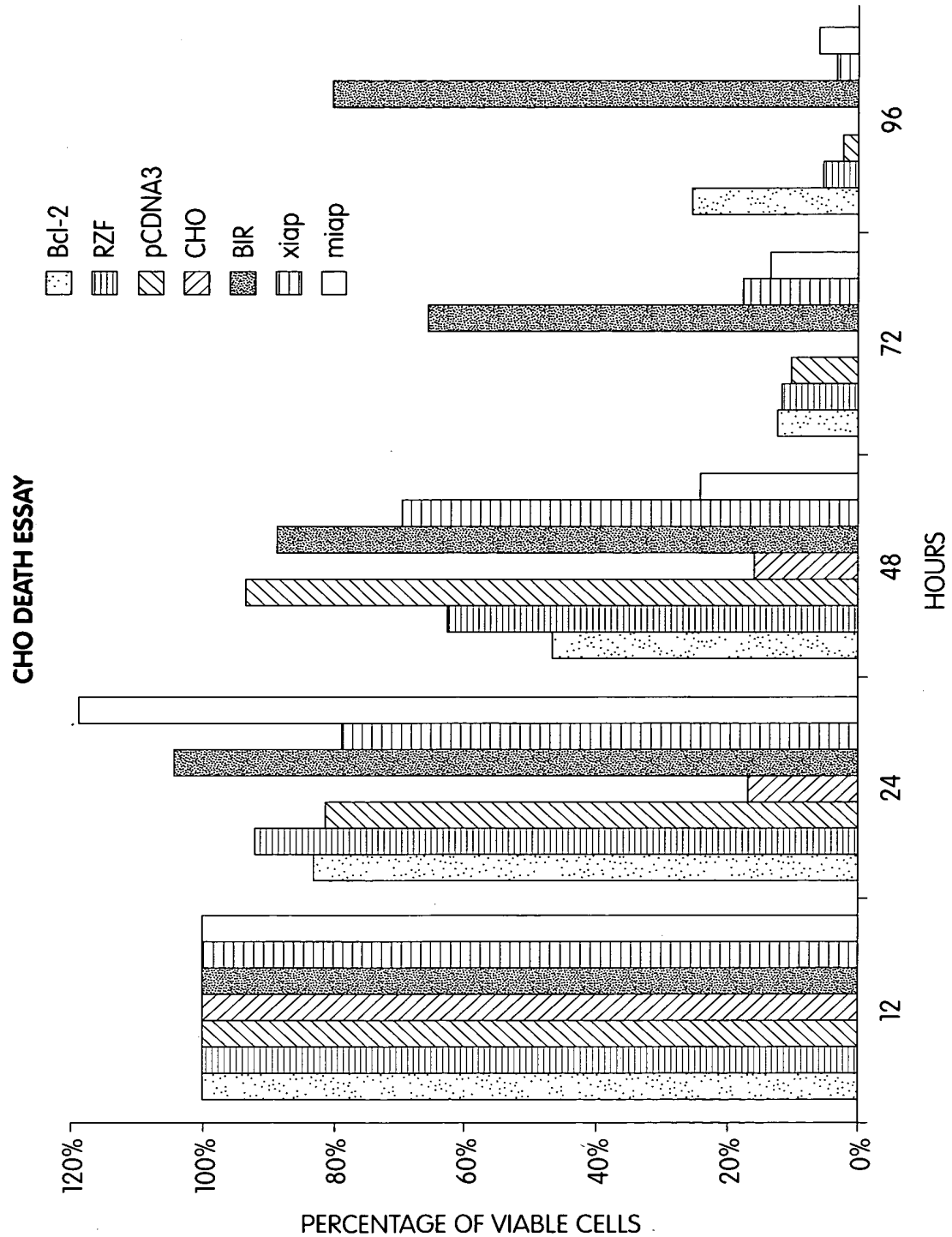


Fig. 14D

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**Fig. 15A**

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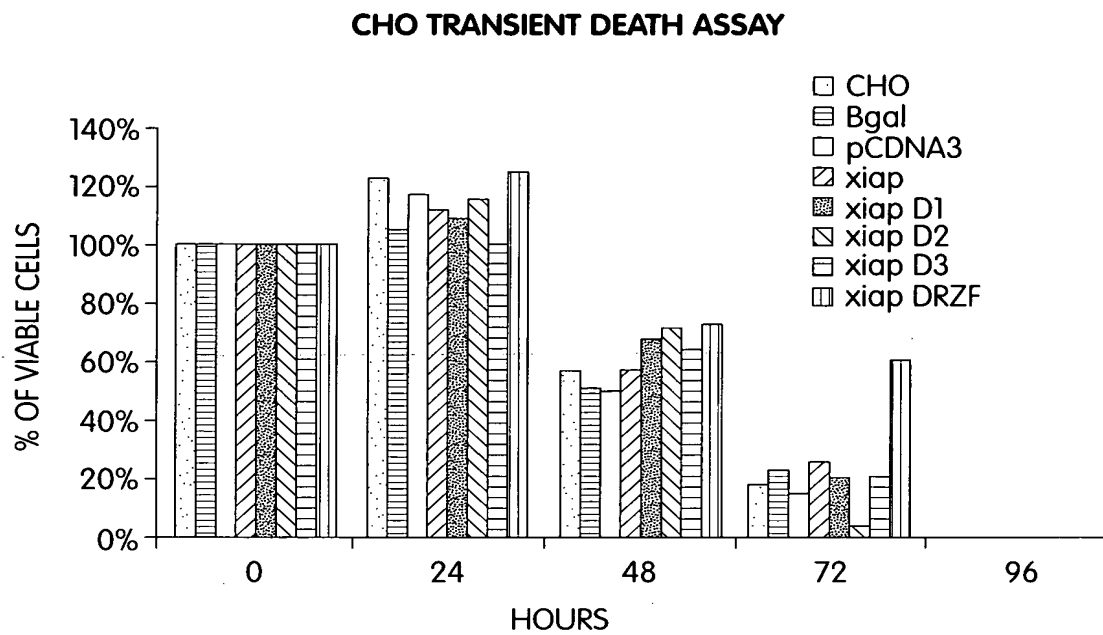


Fig. 15B

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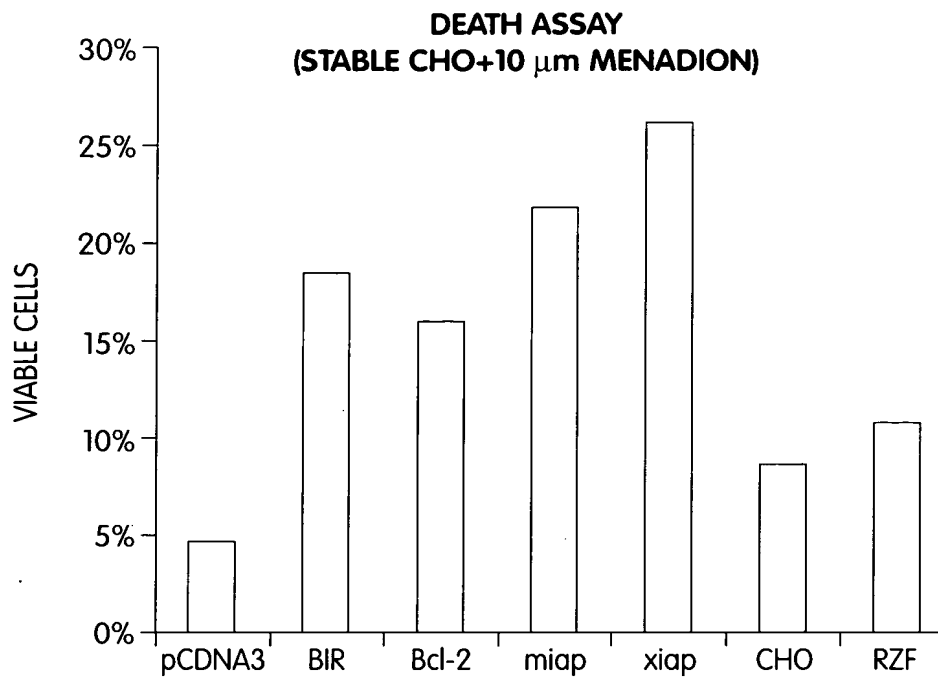


Fig. 16A

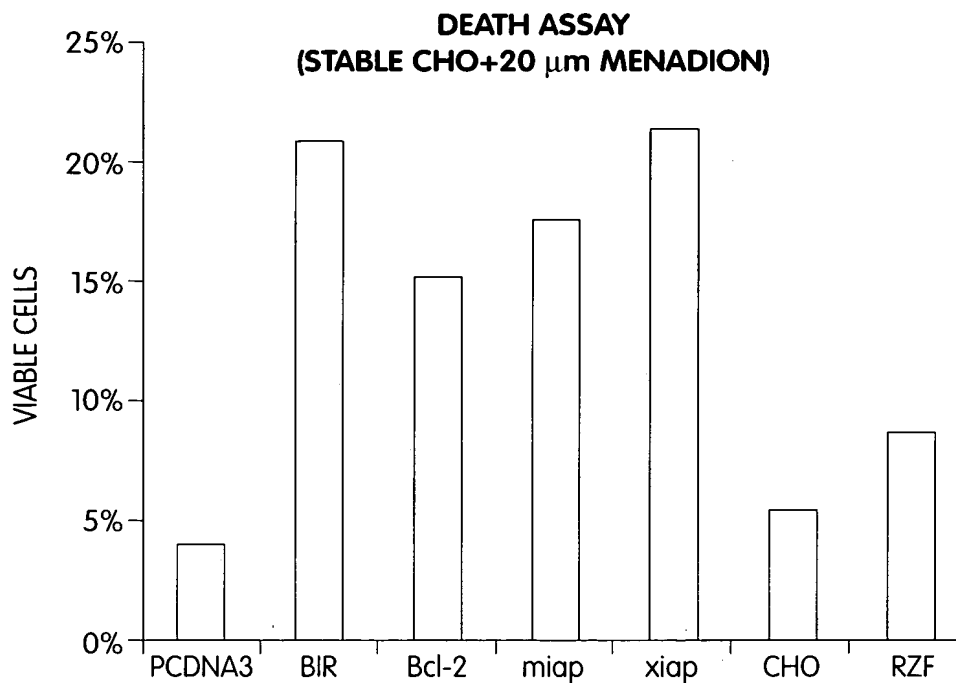


Fig. 16B



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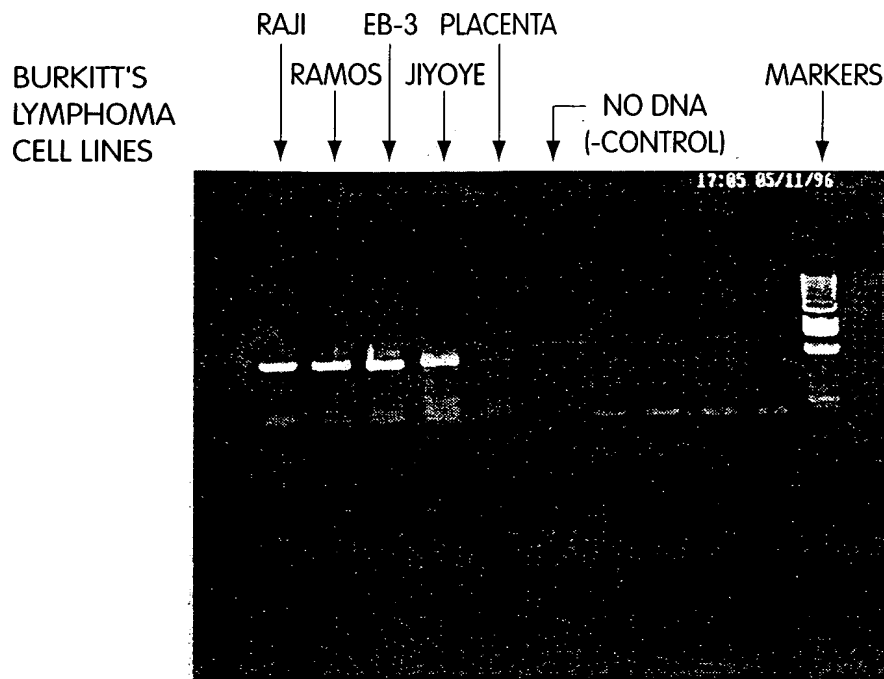


Fig. 17

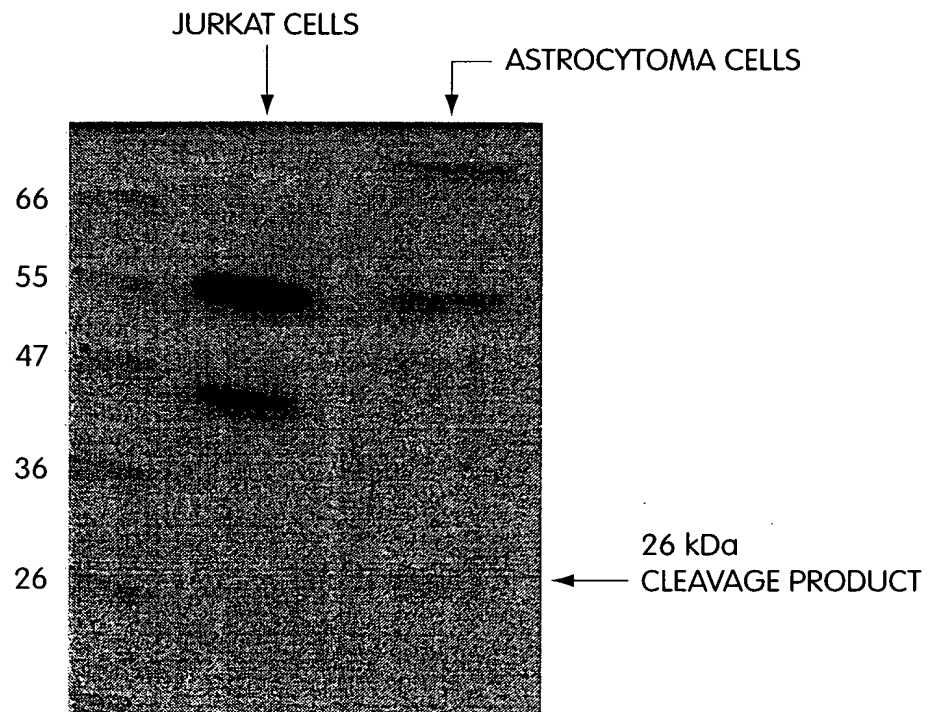


Fig. 18

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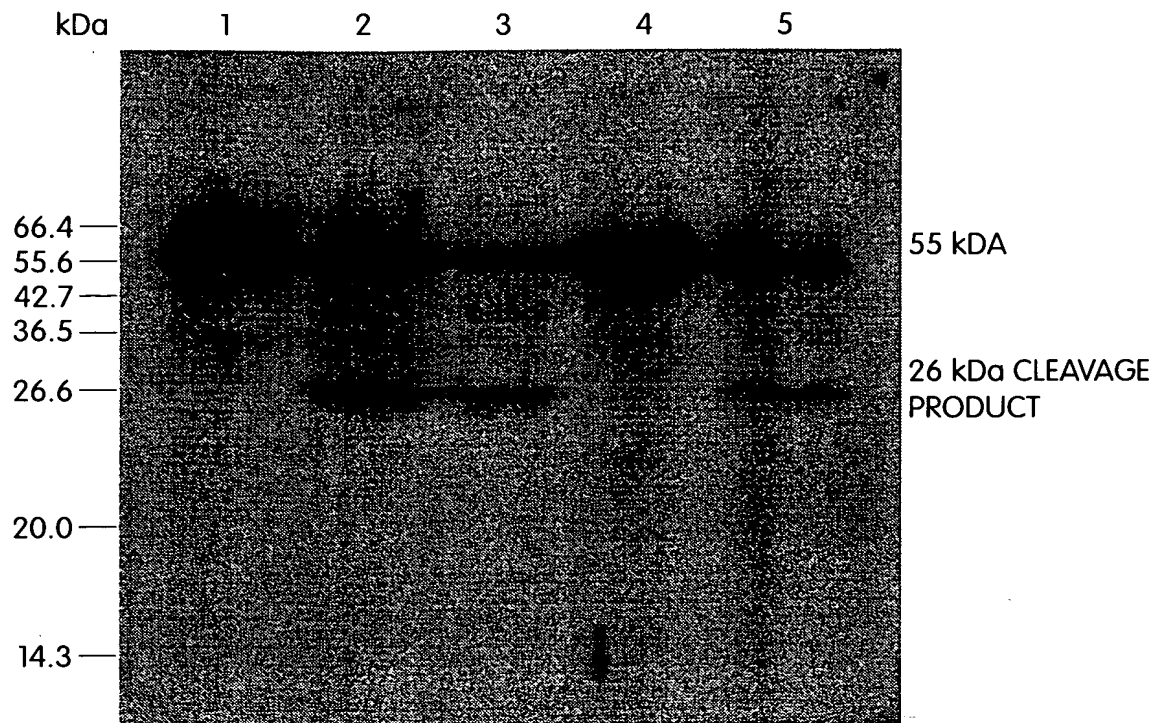


Fig. 19

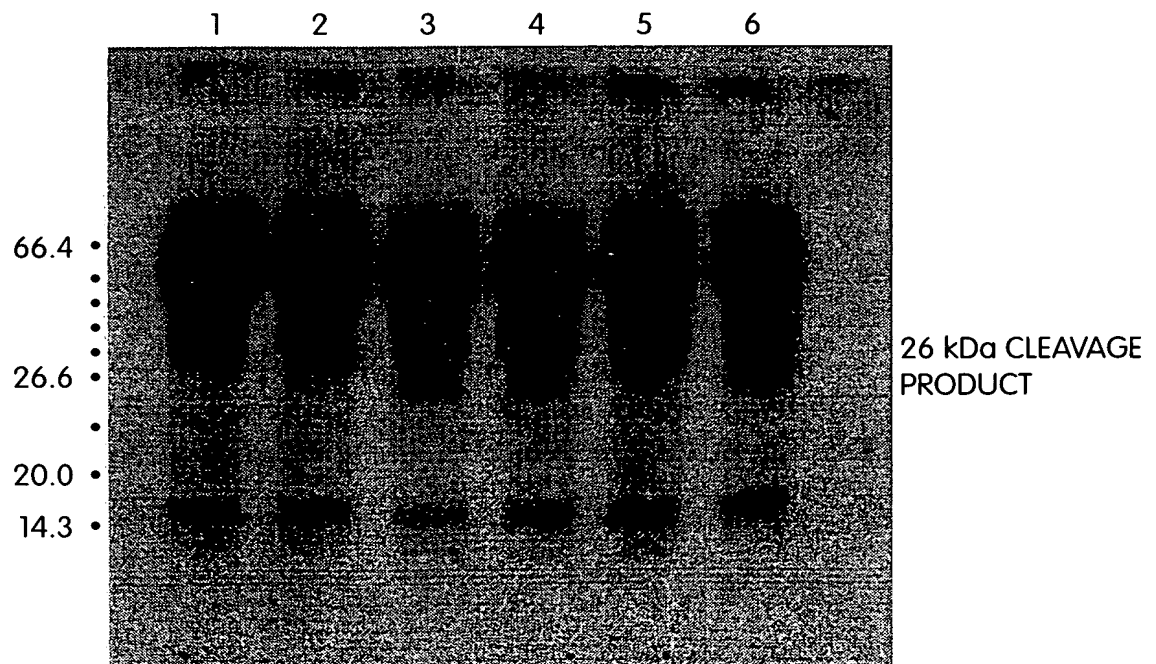


Fig. 20

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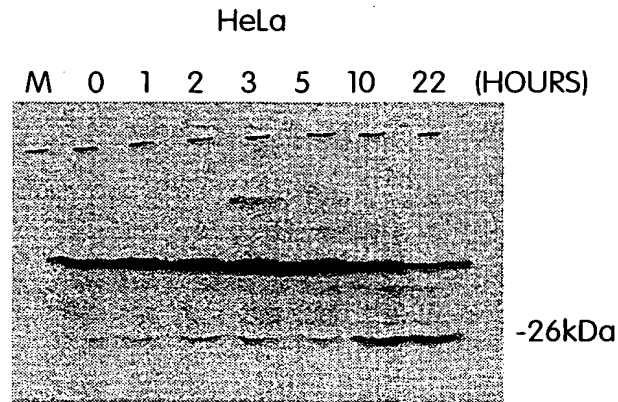


Fig. 21A

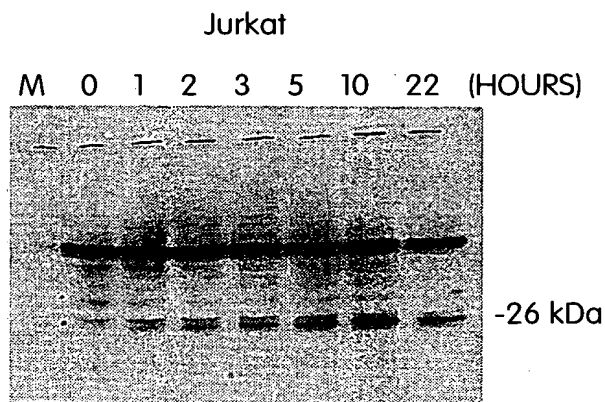


Fig. 21B

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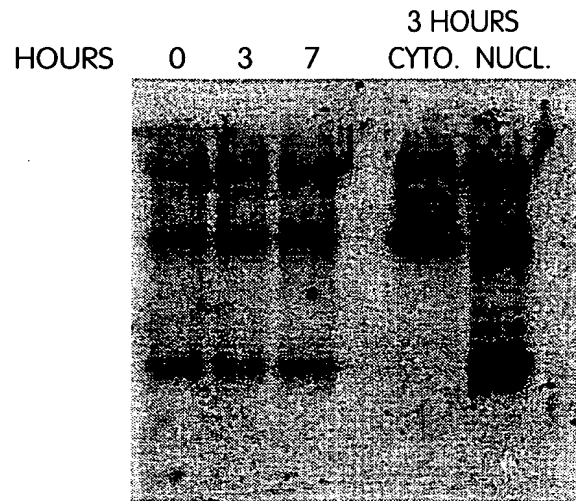


Fig. 22A

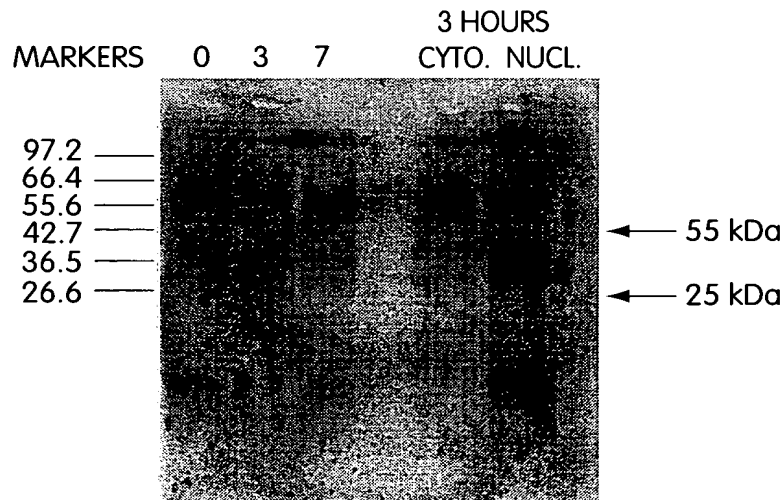


Fig. 22B

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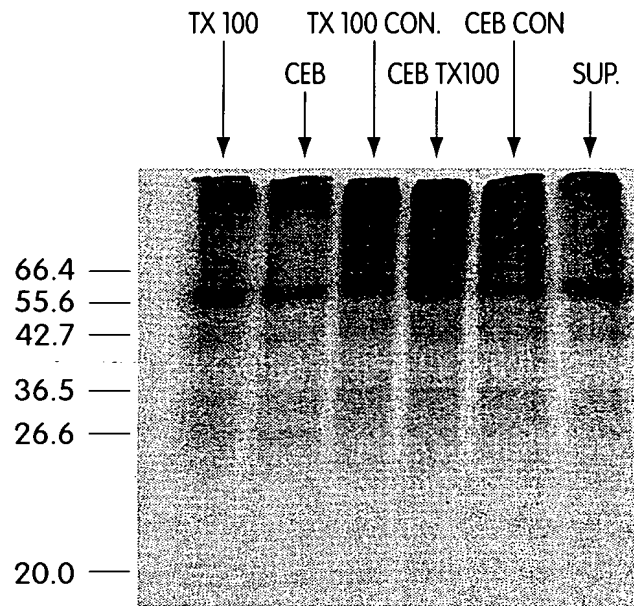


Fig. 23

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